

Genome version 1.4 10/10/98
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OM protein - protein search, using sw model

Run on: March 12, 2003, 04:41:15 : Search time 00:00:29 Seconds
(without alignments)
606 141 Million cell updates/sec

Title: US-09-877-160-1

Perfect score: 653

Sequence: 1 MKETIAFFVATLAVMTVSGE.....GUIDEDLDFPPAPVFNIV 131

Scoring table: BLOSUM62

Gapop 10.0, Gapov 0.5

Searched: 281224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters. 293224

Minimum DB seq length: 0

Maximum hp seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: PIR 73:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	648	97.7	148	2 S06734	allergen, 148
2	90	13.6	185	2 C70199	hypothetical prote
3	87.5	13.2	233	2 E3055A	hypothetical prote
4	87	13.1	249	2 E71865	probable neuramin
5	87	13.1	2197	2 C03817	604K Gal3i complex
6	86.5	13.0	978	2 A70387	conserved hypothet
7	86	13.0	2372	2 T29140	hypothetical prote
8	85.5	12.9	565	2 H83996	DNA repair and gen
9	84	12.7	249	2 B64571	probable neuramin
10	84	12.7	256	2 S58923	tropomyosin isofor
11	83.5	12.6	603	2 H73156	exonuclease AB2 C
12	83	12.5	595	2 S46925	hypothetical prote
13	83	12.5	2245	2 T18278	myosin heavy chain
14	82.5	12.4	233	2 S70371	lik2.11 protein, fi
15	82	12.4	1156	2 H70356	chromosome assembl
16	81.5	12.3	232	2 T46277	hypothetical prote
17	81.5	12.3	445	2 H81341	signal recognition
18	81.5	12.3	484	2 S60947	GMP2 protein - vea
19	81.5	12.3	1979	1 S03166	myosin heavy chain
20	81	12.2	1539	2 A71874	PR-40 Antigen, 14
21	81	12.2	2332	2 T13629	hypothetical prote
22	80.5	12.1	144	2 C69255	hypothetical prote
23	80.5	12.1	159	2 A71137	hypothetical prote
24	80	12.1	784	1 SUEFLA	endopeptidase La
25	80	12.1	784	1 S06890	endopeptidase La
26	80	12.1	784	2 A20684	ion fructose 1,6-b
27	80	12.1	799	2 A85541	hypothetical prote
28	80	12.1	886	2 H60478	conserved hypothet
29	80	12.1	1371	2 T29219	hypothetical prote

30 79.5 12.0 209 2 B93979 conserved hypothet
31 79.5 12.0 309 2 C70325 hypothetical prote
32 79 11.9 166 2 C73342 hypothetical prote
33 79 11.9 554 2 E90601 hypothetical prote
34 79 11.9 559 2 S55282 papilliprictyl iso
35 79 11.9 691 2 G69724 RNA topoisomerase
36 79.5 11.8 234 2 L64016 heat shock protein
37 78.5 11.8 426 2 A44440 estradiol regulated
38 79.5 11.9 449 2 T30406 hypothetical prote
39 78.5 11.9 955 2 C24248 myosin heavy chain
40 78.5 11.8 1975 2 C28173 myosin like protei
41 78.5 11.8 2442 2 T08621 centromere associa
42 78.5 11.9 1329 2 A42771 reticulocyte-bind
43 78 11.8 512 2 C97263 Abc type MK trans
44 78 11.8 448 2 C70375 thiophene and fura
45 78 11.8 536 2 T01870 probable pectinest

ALIGNMENTS

RESULT 1

S06734

allergen, 148 : house dust mite (Dermatophagoides pteronyssinus) (fragment)

N:Alternate names: IgE-binding protein

C:Species: Dermatophagoides pteronyssinus

C.Date: 04-Feb-1990 #Sequence_revision: 04 Feb 1990 #trial_change: 18-Jun-1993

C.Accession: S06734

R:Tovey, P.P.; Johnson, M.C.; Poole, A.L.; Cohen, G.S.; Baldo, R.A.

J. Exp. Med. 170, 1457-1462, 1989

A:Title: Cloning and sequencing of a cDNA expressing a non-oligomer house dust mite prote

A.Reference number: S06734; MUID:50010001; PMID:2794865

A.Accession: S06734

A:Molecule type: mRNA

A:Residues: 1-148 <TOV>

A:Class references: EMBL:X12609

A:Title: the author translated the amino acid residue 118 as Val

Query Match 97.7% Score 648; DB 2; Length 148;

Best Local Similarity 98.5%; Pred. No. 9.4e-44;

Matches 129; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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CY 1 MKETIAFFVATLAVMTVSGE.....GUIDEDLDFPPAPVFNIV 131
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CF 1 MKETIAFFVATLAVMTVSGE.....GUIDEDLDFPPAPVFNIV 131
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CY 1 MKETIAFFVATLAVMTVSGE.....GUIDEDLDFPPAPVFNIV 131
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CF 1 MKETIAFFVATLAVMTVSGE.....GUIDEDLDFPPAPVFNIV 131
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CY 1 MKETIAFFVATLAVMTVSGE.....GUIDEDLDFPPAPVFNIV 131
   |||||
CF 1 MKETIAFFVATLAVMTVSGE.....GUIDEDLDFPPAPVFNIV 131
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RESULT 2

C70199

hypothetical protein E8070c Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C.Date: 11-Feb-1994 #Sequence_revision: 11 Feb 1994 #trial_change: 04-Oct-1999

C.Accession: C70199

R:Prager, C.M.; Gasjens, S.; Huang, W.M.; Sutton, G.O.; Clayton, P.; Lathigra, R.; White

son, D.; Peterson, J.; Fellagaj, A.B.; Gaudemur, S.; Salazar, C.; Hanson, M.; Vagstad,

A. Roman, S.; Saland, S.; Fujii, S.; Saland, S.; Saland, S.; Saland, S.; Saland, S.

Nature 390, 593-597, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A.Reference number: A70100; MUID:50010001; PMID:9403685

A.Accession: C70199

A:Status: Preliminary, nucleic acid sequence not shown, translation not shown

A:Molecule type: DNA

A:Residues: 1-185 <MLE>

A:Title: the author translated the amino acid residue 118 as Val

A:Residues: 143-183 <KAW>

C:Genetics:

A:Date: May 1

A:Inserts: 52/3, 97/2, 136/3, 150/2, 206/3, 230/1

C:Superfamily: Spirochaeta

C:Keywords: alternative splicing

Query Match 12.74, Score 94, DB 2, Length 250,

Best Local Similarity 26.64, Prod. No. 14,

Matches 32; Conservative 25; Mismatches 52; Indels 14; Gaps 4;

QY 17 VCCETVTVVCHVEFLM.....EFHEQIVFRELALFVLQEQI.....CHFEFVTVVFM 27

DB 125 VVACAEKVEYVAPLAVVAAEALAEALAEAGKHVELEEEFVYVGNLCELVSE- 183

QY 28 FPIVAVMCTTIAMTNGVTVVTVVTCVQVPCVTEQVYVLEMLVPTVCTVLEPQVFEAFV 107

DB 184 -EKALQED---SYEQIPTVSSRLKAEATPAEFAERSVQVQLQEVPLDELLLEPERV 239

QY 129 KNI 130

DB 240 RNL 242

RESULT 11

H70156

excinuclease ABC chain C homolog - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C:Date: 13-Sep-1999 #SeqName: revision 13-Sep-1999 #Ext_Change: 20-Apr-2000

C:Accession: H70156

R:Pract: C.M. Casaccia, S. Huang, W.M. Sutton, G.G. Clayton, R. Lathigra, R. White

S:Ref: J. Biol. Chem. 274, 11307-11313, 1999

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S:Ref: J. Biol. Chem. 274, 11307-11313, 1999

S:Ref: J. Biol. Chem. 274, 11307-11313, 1999

bbk2.11 protein precursor - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C:Date: 16 Feb 1997 #sequence_revision 13 Mar 1997 #seq_change 21 Jul 2000
 C:Accession: S70531
 C:Authors: D.B.; Porcella, S.F.; Papova, T.G.; Shevchenko, D.; Baker, S.J.; Li, M.; Morgan
 Mol. Microbiol. 18, 507-520, 1995
 A:Title: Evidence for in vivo but not in vitro expression of a Borrelia burgdorferi outer
 A:Reference number: S70531; MUID:96342380; PMID:8748034
 A:Accession: S70531
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-233 <AK1>
 A:Cross-references: EMBL:U00617; MIM:3309615; PIDM:AAC46421.1; PID:31197933
 F:1 20/Domain: signal sequence #status predicted <SIG>
 F:21-233/Product: bbk2.11 protein #status predicted <MAT>

Query Match 12.48; Score 82.5; DB 2; Length 233;
 Best local similarity 23.61; Pred. No. 17;
 Matches 19; Conservative 27; Mismatches 53; Indels 43; Gaps 7;
 QY 1 MKETIAFFVATIAVMT---VSGEDKHHYQNEEDFLIMERHEQIAKGLALFYLLQEQIN 57
 DB 5 MKMFLICAVFALMSCENYASNEIKNSFN-----LASSSEINVKYTPR---IPYQVF 55
 QY 58 HF-----EETPTMKYKIVAEKMTIIMIDG-----VRCVLD 91
 DB 56 GFLEILETFEDLSKLEETTFEFPQGFILPNKTFPLDSKFTFETVCRVFFVYINVKY 114
 QY 92 LMGQFDIDFQYVLEMLKYSQD---ILEPDKKKEARYK 128
 DB 115 LAGQHFHGFHFFHGFHGFHGFHGFHGFHGFHGFHGFHGFHGFHGFHGFHGFHGFH 155

RESULT 15
 B70356
 chromosome assembly protein homolog - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08 May 1998 #sequence_revision 28 May 1998 #seq_change 22 Jul 2000
 C:Accession: B70356
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lennox, A.L.; Graham, D.E.; Ovi
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196566; PMID:9537320
 A:Accession: B70356
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1156 <AQF>
 A:Cross-references: 38 Acc00642; MIM:3309615; PIDM:AAC46421.1; PID:31197933
 A:Experimental source: strain VF5
 C:Genetics:
 A:Gene: xcpC
 C:Superfamily: chromosome segregation protein SMC1

Query Match 12.48; Score 82; DB 2; Length 1156;
 Best local similarity 26.11; Pred. No. 1802;
 Matches 30; Conservative 24; Mismatches 43; Indels 30; Gaps 5;
 QY 29 EFDELLMERHEQIK-----KQRLALP-VLQFQINHPPEKPTMKYKIVAEKMTIIM 92
 DB 192 EID LILHILNOLKELKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFF 250
 QY 83 DQVRGVLDRL---MQRKLDIFFQYNI-----EMLKKSQDILE 117
 DB 271 LKLLKLLKLLKLLKLLKLLKLLKLLKLLKLLKLLKLLKLLKLLKLLKLLKLLKLL 310
 QY 118 RDLKKKEAPVKNIE 131
 DB 311 RELAESNPENIE 324

Search completed: March 12, 2003, 13:25:48
 Job time : 25.9699 secs

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GenCore version 5.1.4 p5 4578
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Gen protein protein search, using sw model

Run on: March 11, 2003, 15:23:44 ; Search time 16.7759 seconds
(without alignments)
326.353 Million cell updates/sec

Title: US-09-877-160-1

Perfect score: 661

Sequence: 1 MKFTIAPFVATLAVMTVSGE.....GILPDLKYEAPVYEV 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum hit seq length: 400000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	652	99.3	132	1	ALL5_DERPT
2	275.5	41.6	134	1	ALL5_DERPT
3	186	29.1	122	1	ALL5_DERPT
4	96	14.5	896	1	PASO_SULAC
5	86.5	13.0	978	1	PASO_SULAC
6	85.5	12.5	254	1	FMN_DROME
7	85.5	12.9	565	1	RECIN_BACHD
8	84	12.7	1433	1	REST_CHICK
9	81.5	12.6	503	1	UVRB_BOBBU
10	83	12.5	520	1	THB_YEAST
11	83	12.5	2245	1	MYSG_DICDI
12	82.5	12.4	727	1	MPPI_ARATH
13	82.5	12.4	878	1	SYA_THETN
14	82.5	12.4	2236	1	PG4_HUMAN
15	81.5	12.3	1978	1	MYHB_CHICK
16	81	12.2	1072	1	CARB_THETN
17	80.5	12.1	144	1	Y047_APOF
18	80	12.1	784	1	LOX_ECOLI
19	80	12.1	879	1	PA50_SULTO
20	80	12.1	886	1	PA50_APCFU
21	79	11.9	166	1	YB38_MYCPN
22	79	11.9	559	1	PKB7_WHEAT
23	79	11.9	691	1	TCPI_BACSU
24	79	11.9	1972	1	MYHB_HUMAN
25	78.5	11.8	419	1	NEMO_HUMAN
26	78.5	11.8	436	1	EP45_XENLA
27	78.5	11.8	1875	1	MLP1_YEAST
28	78.5	11.8	2869	1	BBP1_PLAUB
29	78	11.8	284	1	TPMM_ANISI
30	78	11.8	448	1	TRME_AQUAE
31	77.5	11.7	578	1	MOEH_DROME
32	77.5	11.7	1055	1	TIRH_HAEIN
33	77.5	11.7	1257	1	FLIH_CASEL

34	77	11.6	845	1	SCD1_MESAU
35	77	11.6	914	1	SYA_PYRAB
36	77	11.6	1730	1	UCO1_YEAST
37	77	11.6	1972	1	MYHB_RABIT
38	76.5	11.5	482	1	PASO_PPFU
39	76.5	11.5	1427	1	REST_HUMAN
40	76	11.5	132	1	KTHY_CAMEL
41	76	11.5	284	1	TPMM_TRICO
42	76	11.5	84	1	PASO_SULTO
43	76	11.5	1163	1	SBAC_GLOBE
44	76	11.5	1263	1	MYHB_HUMAN
45	76	11.5	1679	1	YIC9_YEAST

ALIGNMENTS

RESULT 1
ALL5_DERPT STANDARD; PRT; 132 AA.
AC P14004;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mite allergen Der p 5 (Der p V) (IgE-binding allergen).
GN DERP5.
OC Dermatophagoides pteronyssinus (House dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata, Analgida, Pyroglyphidae;
OC Dermatophagoides.
OX NCBI_TaxID=6956;
PF SEQUENCE FROM N.A.
RX MEDLINE=90010801; PubMed=2704865;
PA Lin K. L., Haieh K. H., Thomas W. R., Chiavv B. L., Chua K. Y.;
RT "Characterization of Der p V allergen, cDNA analysis, and IgE-mediated
RT reactivity to the recombinant protein.";
EL J. Allergy Clin. Immunol. 94:989-996(1994).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=90010801; PubMed=2704865;
PA Torrey P. P., Johnson M. C., Pache A. L., Cohen G. S., Baldo B. A.;
RT "Cloning and sequencing of a cDNA expressing a recombinant house dust
RT mite protein that binds human IgE and corresponds to an important low
RT molecular weight allergen.";
KL J. Exp. Med. 170:1457-1462(1990).
[3]
REVISION TO 132.
PA Cohen G. S.;
EL Subm. 04 (FEB 1994) to the EMBL/Genbank/Trill databases.
CC -1- SIMILARITY: BELONGS TO THE MITE GROUP 5 ALLERGEN FAMILY.
CC This SWISS PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/usage/>,
CC or send an email to license@isb-sib.ch).
CC EMBL; S76337; AAB32841.1;
DR EMBL; S76337; AAB32841.1;
DR EMBL; X17699; CAA35692.1; ALT_INIT.
DR PIR; S06734; S06734.
KW Allergen.
FT VARIANT 61 61 15615 MW; 3046072570705 CRC64;
SQ SEQUENCE 132 AA; 15615 MW; 3046072570705 CRC64;
Query Match 98.3%; Score 652; DB 1; Length 132;
Best Local Similarity 98.5%; Pred. No. 9e-45;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cv 1 MFTIAPFVATLAVMTVSGE.....GILPDLKYEAPVYEV 132


```

RESULT 7
REC# EACH#
ID REC# BACHD STANDARD; PRT; 565 AA.
AC 064374;
DT 16-OCT-2001 (rel 40, Created)
DT 16-OCT-2001 (rel 40, Last sequence update)
DT 16-OCT-2001 (rel 40, Last annotation update)
DE DNA repair factor RCH (PREDICTION ERROR)
REC# BACHD#
G# Facilities Managers

```

RESULT 8	
REST CHECK	
ID	REST CHECK
DD	STANDARD; PPT: 1433 AA.
DT	-41124, 41124, 41124, 41124
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	15-JUN-2000 (Rel. 41, Last annotation update)
DT	Position (Cytochrome b) Inter Protein-170 (CytP-170).
GN	RSN
GN	Gallus gallus (Chicken)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Aves; Neognathae; Galliformes; Gallinidae; Phasianidae;
OC	Gallus
OC	NCBI TaxID=9031;
OC	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=9813792; PubMed=9459933;
RX	Gripatic L., Volcsky D.M., Keller T.C. III;
RX	"cloning and expression of chicken CytP-170 and related isoforms";
EL	Gene 336:195-209 (1998).

SEQUENCE OF 17,119 FROM N.A. (ISOFORMS 3 AND 4).
 (21)
 RP
 EC
 TISSUE
 PC
 PA
 GP
 FT
 PL
 (22)


```

DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_Tail.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001509; myosin_head.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR Pfam; PF02716; Myosin_N; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS0096; IQ; 1.
KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW ATP-binding; Methylation; Alkylation; Calmodulin-binding;
KW Multigene family; 3D-structure.
FT INIT MET 0 0
FT DOMAIN 1 790 MYOSIN HEAD-LIKE.
FT DOMAIN 791 820 IQ.
FT DOMAIN 849 1978 RODLIKE TAIL (S2 AND IMM DOMAINS).
FT DOMAIN 849 1578 COILED COIL (POTENTIAL).
FT NP_RIND 176 183 ATP.
FT DOMAIN 666 688 ACTIN-BINDING.
FT DOMAIN 767 781 ACTIN-BINDING.
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 127 127 METHYLATION (TR1) (POTENTIAL).
FT MOD_RES 706 706 ALKYLATION (SH-1).
FT MOD_RES 716 716 ALKYLATION (SH-2).
FT CONFLICT 127 127 MISSING (IN REF. 3).
FT CONFLICT 204 215 KUISITQSPFS->RIFASLKVHLFP (IN REF. 1).
SQ SEQUENCE 1978 AA; 43865 MW; 57665355C77C93 CRC64;

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Query Match 12.38; Score 81.5; DB 1; Length 1978;
 Best Local Similarity 27.28; Pred. No. 77;
 Matches 34; Conservative 27; Mismatches 47; Indels 17; Gaps 7;

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Q1 14 LAKMIVGDELKAKTLEKPPILMKPILKLPVDFIALFYLDGKINHHKPKT.....KE 66
   |||||
Db 1371 ISTLIQLSDSPVWQ-PET-ATVETWEEGPPHQPSPSLTCC FEEYAAAYGVLEK 1425
   |||||
Q2 67 MEDIVAFPMQTIAMITGVVPIPIWPPY MDIFECYNLEMLKPPSCLLEKPKVE 103
   |||||
Db 1425 IANLGLFIIAGGVLELINPLVSNLEKPKKPSLWLAEEFNIS--SYAD EEPDAEA 1491
   |||||
Q3 124 EARK 128
   |||||
Db 1482 EAREK 1486

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Search completed: March 12, 2003, 08:52:03
 Job time : 20.7759 secs


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Best local similarity: 22.69, Pct Id: 2.4,
Matches: 29, Conservative: 23, Mismatches: 36, Indels: 10, Gaps: 3;

QY 15 MERHETGIVGELALFYCEGHNHFEETPTETEMFTVAEMDTIAMIAPVSVLPELWQ 94
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DR 1700 LRFEPFEPFAPFAPFAPFAPFAPFAPFAPFAPFAPFAPFAPFAPFAPFAPF 1790
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 95 PELLIFE-QYNLEMLKSSGILLERLKEEAPVNIIE 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DR 1791 PLEPVAAPVNIIEFAPVYSPCTAPPAAPVAPVAPVAPVAPVAPVAPVAPV 1919

RESULT 2
Q42351 PRELIMINARY; PRT: 860 AA.
ID O42351
AC O42351
DT 01-JAN-1998 (Tremblrel. 05, Created)
DI C: "AN: 1998 (Tremblrel. 05, Last sequence update)"
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Chicken PARABOLIN A, NEMPHOGENIN
OS Gallus Gallus (Chicken)
OC Euryarchaea, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
OC Gallus
OX NCBI_Taxid=9031;
PN 11
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Nishimuro H., Oyeda A., Nishimuro H., Taguchi T.;
RL Submitted (Nov-1998) to the EMBL/Genbank/CCLE databases
RE SEQUENCE OF 79-860 FROM N.A.
RC TISSUE=MUSCLE, AND TELENCEPHALON;
RX MEDLINE=1975215; PubMed 3427343;
RA Nishimuro H., Oyeda A., Nishimuro H., Taguchi T.;
RT "Neurorescin: a novel neurite-outgrowth factor secreted by muscle
RT after denervation";
RL NeuroReport 8:2649-2654 (1997)
DE FMS: 2649-2654, PAA11757 1;
DR EMBL: D38038, PAA23805 1;
DR InterPro: IP001014; PARABOLIN
DE Pfam: PF03529; PARABOLIN; 2;
DR PRINTS: PP01432; PARABOLIN
SQ SEQUENCE 860 AA, 29414 MW, 20052222.438 DGE CRC61,

Query Match 15.18, Score 100, DB 13, Length 860,
Best local similarity 29.68, Pct Id: 5,
Matches: 40, Conservative: 26, Mismatches: 45, Indels: 24, Gaps: 9;

QY 16 TSGCGDYH-QYONREPLIMPTHTPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTV 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 648 STGCHSHSVSTGCHSHSVSTGCHSHSVSTGCHSHSVSTGCHSHSVSTGCHSHSV 768
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 17 MPTHTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTV 104
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 706 PPTHTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTV 768
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 18 MPTHTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTV 104
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 766 PPTHTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTV 768
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
Q42351 PRELIMINARY; PRT: 846 AA.
ID O75130
AC O75130
DT 01-NOV-1998 (Tremblrel. 08, Created)
DI 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE KIAA0635 protein.
GN KIAA0635
OS Homo sapiens (Human)
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=9841980; PubMed 9734911;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176 (1998).
DR EMBL: AB014535; BAA31610.1;
SQ SEQUENCE 846 AA, 29213 MW, 20052222.438 DGE CRC64;

Query Match 14.28, Score 94.5, DB 4, Length 846;
Best local similarity 25.28, Pct Id: 14;
Matches: 29, Conservative: 26, Mismatches: 40, Indels: 10, Gaps: 4;

QY 93 QYVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 636 LLELLELLELLELLELLELLELLELLELLELLELLELLELLELLELLELLEL 660
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 93 QYVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DE 691 DOCKPTNTGQVNSVPLPPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTV 740
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
Q404011 PRELIMINARY; PRT: 459 AA.
ID Q404011
AC Q404011
DT 01-NOV-1996 (Tremblrel. 01, Created)
DI 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Myosin-like protein (fragment).
GN MYOSIN-LIKE PROTEIN.
OS Wuchereria bancrofti.
RX PubMed 13122399, PubMed 19573386;
RA Baghavan N., McPeckolde L.A., Maida C.V., Peinerone S.M.,
RA Jayaraman K., Ottosen E.A., Numan T.B.;
RT "A recombinant clone of Wuchereria bancrofti with DNA specificity for
RT human lymphatic filarial parasites";
RL Mol. Biochem. Parasitol. 47:63-71 (1991).
DR EMBL: M9013; AAA61560 1;
SQ SEQUENCE 459 AA, 53314 MW, 55433333.862 DGE CRC64;

Query Match 14.18, Score 93.5, DB 5, Length 459;
Best local similarity 26.28, Pct Id: 8.5;
Matches: 39, Conservative: 26, Mismatches: 40, Indels: 10, Gaps: 6;

QY 11 THTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTV 77
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 41 THTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTV 95
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 IIAI--IDGVEGVLDIMQVPLDIEE-QYNLEMLKSSGILLERLKEEAPVNIIE 124
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 36 LIANEVQLHSLIIIFISALNIEETELLENLEHLEHLEHLEHLEHLEHLEHLEH 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 125 ARVNI 130
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 154 KIMQNV 161
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
Q97195 PRELIMINARY; PRT: 311 AA.
ID Q97195

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OY NCBI_TaxID:3055;
RN [1]
RF SEQUENCE FROM N.A.
RX PubMed:1197094;
RA Tam L.W., Lefebvre P.A.;
PT "The Chlamydomonas MBOC locus encodes a conserved coiled-coil protein
  important for flagellar waveform conversion";
RL Cell Motil. Cytoskeleton 51:137-152(2002);
DR EMBL; AF394181; AAM15711.1; ;
KW Flagella.
W 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 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GenCore version 5.1.4 p5 4578
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CM protein - protein search, using sw model

Run on: March 11, 2003, 16:11:59 : Search time 31.3311 seconds
(without alignment)
527,708 Million cell updates/sec

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Perfect score: 63
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Scoring table: BLOSUM62

Gapop 10.0, Gapext 5.5

Searched: 90470 seqs, 1000000 residues

Total number of hits satisfying chosen parameters 90470

Minimum DB seq length: 0

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	275.5	41.5	134	22	Domestic mite Bt5
3	275.5	41.6	134	23	Blomia tropicalis
4	275.5	41.6	134	23	Blomia tropicalis
5	270.5	40.8	134	22	Domestic mite Bt5
6	270.5	40.8	134	22	Blomia tropicalis
7	264	39.9	127	22	Domestic mite Bt5
8	264	39.8	127	22	Blomia tropicalis
9	263	39.7	127	22	Colombian mite Bt5
10	263	39.7	127	23	Blomia tropicalis

11	263	39.7	117	23	Blomia tropicalis
12	261	39.4	117	22	Domestic mite Bt5
13	261	39.4	117	22	Domestic mite Bt5
14	261	39.4	117	22	Domestic Bt5 polym
15	261	39.4	117	23	Blomia tropicalis
16	261	39.4	117	23	Blomia tropicalis
17	255	38.5	117	22	Colombian mite Bt5
18	255	38.5	117	22	Singapore mite Bt5
19	255	38.5	117	23	Blomia tropicalis
20	255	38.5	117	23	Blomia tropicalis
21	178	26.8	84	22	Domestic mite Bt5
22	178	26.8	84	22	Blomia tropicalis
23	160	15.1	782	23	Blomia tropicalis
24	97	14.0	687	17	Blomia tropicalis
25	95.5	14.4	596	23	Blomia tropicalis
26	95.5	14.4	596	23	Blomia tropicalis
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28	87	13.1	549	18	Blomia tropicalis
29	87	13.1	549	18	Blomia tropicalis
30	86	13.0	549	18	Blomia tropicalis
31	85.5	12.9	549	18	Blomia tropicalis
32	85	12.9	549	18	Blomia tropicalis
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ALIGNMENTS

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XX WPI; 2002-195803/25.
 DR N-PSDB; AAD30707.
 XX
 PT Novel immunogenic protein isolated from domestic mite allergen, Blomia
 PT tropicalis, useful for preventing, reducing and ameliorating a
 PT polymorphic Bt5 hypersensitivity
 XX
 XX Claim 4; Page 91; 101pp; English.
 PS
 VV The present invention relates to an isolated immunogenic polymorphic Bt5
 CC protein derived from domestic mite allergen, Blomia tropicalis (Bt). Bt5
 CC is useful for preventing, reducing and ameliorating a polymorphic Bt5
 CC hypersensitivity. Bt5 is used as vaccine and for modulating an immune
 CC response. Bt5 is useful for detecting antibody directed to all or part of
 CC polymorphic Bt5 in a biological sample, from a subject, by contacting the
 CC biological sample with Bt5, its derivative, homologue, analogue, mimetic
 CC or chemical equivalent, to form an antibody-protein complex and detecting
 CC the complex. Bt5 is useful for the prophylactic treatment of an allergic
 CC condition (including allergic asthma, atopic dermatitis and/or rhinitis)
 CC in an individual, e.g. human or animal, by administering Bt5 (preferably
 CC in the form of an eukaryotic expression plasmid vector administered in a
 CC pharmaceutical composition comprising a normal saline or liposome as
 CC carrier), its derivative or homologue, where the airway hyper-reactivity or
 CC airway inflammation is prevented. Bt5 gene is useful in gene therapy. The
 CC present sequence is Blomia tropicalis Bt5 polymorphic amino acid variant
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 SQ Sequence 134 AA;
 Query Match 41.6%, Score 275.5, DB 23, Length 134,
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 Q1 1 MEF 11AEEVATLAWTVLSECEPPEKQKREFFILDMELHNEQIPPEGSALEFYVLEQIN 67
 Db 1 MEALVLLA.FAA SVLALEHREFFTFPEEFCHILLIEYANNAHDEGEMLYVLAHLLE 68
 Q2 58 HFEETPEKEMETVAEMETIAAMISNVSVEELKMSVLELLIEFYELMLMPSGSDILE 117
 Db 59 ELNENPEPEFFETFEITVWAMITFASDALEEFETETENLEEFVEEAELILEHLL 118
 Q3 118 POLKVEAPVNVIE 131
 Db 119 KRLAEIKLVVQIQ 132
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 AAE19386
 ID AAE19386 standard; Protein; 134 AA.
 XX
 AC AAE19386;
 XX
 DT 21 MAY 2002 (first entry)
 DE Blomia tropicalis Bt5 amino acid sequence.
 KW Immunogenic polymorphic Bt5 protein; domestic mite allergen; rhinitis;
 KW hypersensitivity; immune response; allergy; asthma; atopic dermatitis;
 KW pharmaceutical composition; antiallergic; antiasthmatic; dermatological;
 KW antiinflammatory; vaccine; gene therapy.
 XX
 OS Blomia tropicalis.
 VV WO200206323-A1.
 XX
 XX 24-JAN-2002.
 XX
 XX 10 OCT-2000; 2000WO-AU91228.
 XX
 XX 18-JUL-2000; 2000AU-0000445
 XX
 XX (US) ; UNIV SINGAPORE NAT.

PI Chua KY, Cheong N, Lee BW, Liew LN;
 DR WPI; 2002-195803/25.
 XX
 PT Novel immunogenic protein isolated from domestic mite allergen, Blomia
 PT tropicalis, useful for preventing, reducing and ameliorating a
 PT polymorphic Bt5 hypersensitivity
 XX
 XX Disclosure; Fig 3; 101pp; English.
 PS
 VV The present invention relates to an isolated immunogenic polymorphic Bt5
 CC protein derived from domestic mite allergen, Blomia tropicalis (Bt). Bt5
 CC is useful for preventing, reducing and ameliorating a polymorphic Bt5
 CC hypersensitivity. Bt5 is used as vaccine and for modulating an immune
 CC response. Bt5 is useful for detecting antibody directed to all or part of
 CC polymorphic Bt5 in a biological sample, from a subject, by contacting the
 CC biological sample with Bt5, its derivative, homologue, analogue, mimetic
 CC or chemical equivalent, to form an antibody-protein complex and detecting
 CC the complex. Bt5 is useful for the prophylactic treatment of an allergic
 CC condition (including allergic asthma, atopic dermatitis and/or rhinitis)
 CC in an individual, e.g. human or animal, by administering Bt5 (preferably
 CC in the form of an eukaryotic expression plasmid vector administered in a
 CC pharmaceutical composition comprising a normal saline or liposome as
 CC carrier), its derivative or homologue, where the airway hyper-reactivity or
 CC airway inflammation is prevented. Bt5 gene is useful in gene therapy. The
 CC present sequence is Blomia tropicalis Bt5 amino acid sequence.
 XX
 SQ Sequence 134 AA;
 Query Match 41.6%, Score 275.5, DB 23, Length 134,
 Best Local Similarity 42.5%, Pred. No. 2 and 20;
 Matches 57, Conservative 33, Mismatches 39, Indels 5, Gaps 4;
 Q1 1 MEF 11AEEVATLAWTVLSECEPPEKQKREFFILDMELHNEQIPPEGSALEFYVLEQIN 67
 Db 1 MEALVLLA.FAA SVLALEHREFFTFPEEFCHILLIEYANNAHDEGEMLYVLAHLLE 68
 Q2 58 HFEETPEKEMETVAEMETIAAMISNVSVEELKMSVLELLIEFYELMLMPSGSDILE 117
 Db 59 ELNENPEPEFFETFEITVWAMITFASDALEEFETETENLEEFVEEAELILEHLL 118
 Q3 118 POLKVEAPVNVIE 131
 Db 119 KRLAEIKLVVQIQ 132
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 RESULT 5
 AAE02256
 ID AAE02256 standard; Protein; 134 AA.
 XX
 AC AAE02256;
 XX
 DT 31 JUL 2001 (first entry)
 DE Domestic mite Bt5 polymorphic amino acid variant no.24.
 KW Mite; immunogenic protein; Bt5 allergen; therapy; atopic dermatitis;
 KW immediate hypersensitivity; systemic anaphylaxis; allergic rhinitis;
 KW asthma; antiallergic; antiinflammatory; immunosuppressive.
 XX
 OS Blomia tropicalis.
 VV WO200130817-A1.
 XX
 XX 03-MAY-2001.
 XX
 XX 10-OCT-2000; 2000WO-AU01227.
 XX
 XX 26 OCT-2000; 9933-0305313.
 XX
 XX 18-JUL-2000; 2000AU-0008842.
 XX
 XX 18-JUL-2000; 2000AU-0008844.
 XX
 XX 18-JUL-2000; 2000AU-0008845.

[illegible]

Immunogenic polypeptide Bt5 protein, domestic mite allergen; rhinitis; hypersensitivity; immune response; allergy; asthma; atopic dermatitis; pharmaceutical composition; antiallergic; antiasthmatic; dermatological; antiinflammatory; vaccine; gene therapy.

Blomia tropicalis.

WO200206123-A1.

24 JAN-2002.

10-001-2000; 2000W0-A001228.

18 JUL-2000; 2000AU-0008845.

(UNSI) UNIV SINGAPORE NAT.

Chua KY, Cheong N, Lee BW, Liew LN;

WPI; 2002-195803/25.

N FSDR; AAD30694.

Novel immunogenic protein isolated from domestic mite allergen, Blomia tropicalis, useful for preventing, reducing and ameliorating a polypeptide Bt5 hypersensitivity.

Disclosure; Page 77-78; 101pp; English.

The present invention relates to an isolated immunogenic polypeptide Bt5 protein derived from domestic mite allergen, Blomia tropicalis (Bt). Bt5 is useful for preventing, reducing and ameliorating a polypeptide Bt5 hypersensitivity. Bt5 is used as vaccine and for modulating an immune response. Bt5 is useful for detecting antibody directed to all or part of polypeptide Bt5 in a biological sample, from a subject, by contacting the biological sample with Bt5, its derivative, homologue, analogue, mimetic or chemical equivalent, to form an antibody-protein complex and detecting the complex. Bt5 is useful for the prophylactic treatment of an allergic condition (including allergic asthma, atopic dermatitis and/or rhinitis) in an individual, e.g. human or animal, by administering Bt5 (preferably in the form of an eukaryotic expression plasmid vector administered in a pharmaceutical composition comprising a normal saline or liposome as carrier), its derivative or homologue, where the airway hyper-reactivity or airway inflammation is prevented. Bt5 gene is useful in gene therapy. The present sequence is Blomia tropicalis Bt5 amino acid sequence (ref 12).

Sequence 117 AA;

Query Match 39.4%; Score 261; DB 23; Length 117;
Best Local Similarity 44.5%, E-Value 7.1e-10;
Matches 49; Conservative 29; Mismatches 32; Indels 0; Gaps 0;

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DB 6 KKQGFNFEHLLIQANHALEKHEHGLLYVQLDELNENKSKQLQKIPQLDVCAM 65

QV 82 IDGVPGVLDRLMOPKLDIFQVNLPMVKKSGDILRDLKYEAPVNTIE 131

DB 66 IEGAGALELREKPTDNLILERNVEEAQTIKTLKQIPETQPKQIO 115

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Query Match 12.0%; Score 79.5; DB 19; Length 209;
Best Local Similarity 28.3%; Pred. No. 1.4;
Matches 39; Conservative 24; Mismatches 46; Indels 29; Gaps 9;

QY 1 MKF--IIAFVAILAVMIVSGCKKH--QVNEPQGLMPPKHEIIF--ELALFVLDEI 56
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEPEETATVAGVLLAGSTTFFRFAVYFV 51
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 57 NHEERTHEMALVAEM:III AMIDSVPSVIRPMLPHELDIFQVYNLEMLKSS 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 52 AELDEREFTED VNCPTAVPGRVAVTIIPTNATRIE... PEKEE DAIKES- 101
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 114 LILERDLKKAFAVKNIE 131
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 102 -EQDFFAKSHVDNID 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US 09-927-597-2
; Sequence 2, Application US/09-927-597
; Publication No. US2003032018A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Fady
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; APPLICANT: Craven, Andrew
; APPLICANT: Sakowitz, Roman
; APPLICANT: Hartman, James
; TITLE OF INVENTION: Human smooth muscle myosin heavy chain
; FILE REFERENCE: CYTOP018
; CURRENT APPLICATION NUMBER: US/09/927,597
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1945
; TYPE: PRT
; ORGANISM: Human
; US 09-927-597-2

Query Match 11.9%; Score 79; DB 9; Length 1945;
Best Local Similarity 25.8%; Pred. No. 2;
Matches 33; Conservative 28; Mismatches 47; Indels 20; Gaps 7;

QY 9 VALLAVMTVSSEKHYEYNEESFLMREHICIGKISGLAFYLCQVNHHEEPT 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1373 ISTERLQSEFFFAQFSA... -TVFAIRSSKFFAFPHSLITL 1424
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 65 -KEMKQIVAEETIIAMIDSVPSVIRPMLPHELDIFQVYNLEMLKSSGILDERUL 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1425 LEFTPSPGAEFLGQVVLQVNLNLSQVAVNLS...PFTGLAFENLS 1490
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 KFFPAPVW 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1481 AEAAREK 1488
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US 09-927-597-4
; Sequence 4, Application US/09-927-597
; Publication No. US2003032018A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Fady
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; APPLICANT: Craven, Andrew
; APPLICANT: Sakowitz, Roman
; APPLICANT: Hartman, James
; TITLE OF INVENTION: Human smooth muscle myosin heavy chain
; FILE REFERENCE: CYTOP018
; CURRENT APPLICATION NUMBER: US/09/927,597
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 17
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1979
; TYPE: PRT
; ORGANISM: Human
; US 09-927-597-4

Query Match 11.9%; Score 79; DB 9; Length 1979;
Best Local Similarity 25.8%; Pred. No. 2;
Matches 33; Conservative 28; Mismatches 47; Indels 20; Gaps 7;

QY 9 VALLAVMTVSSEKHYEYNEESFLMREHICIGKISGLAFYLCQVNHHEEPT 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1373 ISTERLQSEFFFAQFSA... -TVFAIRSSKFFAFPHSLITL 1424
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 65 -KEMKQIVAEETIIAMIDSVPSVIRPMLPHELDIFQVYNLEMLKSSGILDERUL 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1425 LEFTPSPGAEFLGQVVLQVNLNLSQVAVNLS...PFTGLAFENLS 1490
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 KFFPAPVW 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1481 AEAAREK 1488
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US 09-863-049A-2
; Sequence 2, Application US/09-863-049A
; Publication No. US2003032055A1
; GENERAL INFORMATION:
; APPLICANT: Kenrick, Sue J.
; APPLICANT: Nelson, David L.
; APPLICANT: Aradhya, Swaroop
; APPLICANT: D'Urso, Michele
; APPLICANT: Wofford, Hayley
; APPLICANT: Munnich, Arnold
; APPLICANT: Smahi, Asmaa
; APPLICANT: Israel, Alain
; APPLICANT: Poustka, Annemarie
; APPLICANT: Lewis, Richard A
; APPLICANT: Levy, Moise
; APPLICANT: Heiss, Nina
; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Def
; TITLE OF INVENTION: SYNTAXA B (HIF-2B) Activation
; FILE REFERENCE: HO-P019610S1
; CURRENT APPLICATION NUMBER: US/09/863,049A
; CURRENT FILING DATE: 2001-05-22
; PCT APPLICATION NUMBER: US 65/256,223
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: human
; US 09-863-049A-2

Query Match 11.8%; Score 78.5; DB 9; Length 419;
Best Local Similarity 24.6%; Pred. No. 4.2;
Matches 31; Conservative 27; Mismatches 49; Indels 19; Gaps 4;

QY 1P TVSEDFPHFYCNFFFLMPPKHEIIF--ELALFVLDEI...EPTHEMLE 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 EVVLSSEFP NM.....PFTGLAFENLSQVAVNLS...PFTGLAFENLS 400
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 71 IVAEMDTIIMIDSVPSVIRPMLPHELDIFQVYNLEMLKSSGILDERUL...BEAR 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 LPAALVFAALVAPVAVPEVIAAE... 1424
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 127 VNIEV 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 KRHYEV 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 9

US-09-815-242-11217
 Sequence 11217, Application US/09815242
 Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xia, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA-011A

CURRENT FILING DATE: 2001-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,949

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,579

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/267,931

PRIOR FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14119

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 11217

LENGTH: 1055

TYPE: PRT

ORGANISM: Haemophilus influenzae

US-09-815-242-11217

Query Match

Best local similarity 11.74; Score 77.5; DB 10; Length 1055

Matches 42; Conservative 24; Mismatches 49; Indels 39; Gaps 9;

QY 5 IAFVATVAVTVSUGPHVYVREFQVLMESVDEQVVFSLALVYL.....US-1116F 64

Db 917 IAFVAVPAVIRVPPRAFTGIRVQVQLLPVLRVQVIGDVVQLLELLEPEFQVLL 674

QY 60 IER FVEMKIVAEETIA...MIDGVSVLDELKMPFQVPEQV 134

Db 575 GEEFIVTVDITL...WVAGMSYLACIRPVVSGVSTLQVTFEFPFPMINQVHSH 351

QY 106 NI.....EMKYSQTHLP.....LUPPE 124

Db 524 KLVVLELLEFVQVQVLELALGRLDLFREE 905

RESULT 10

US-09-124-233-12

Sequence 12, Application US/09134333

Patent No. US20030076403A

GENERAL INFORMATION:

APPLICANT: LONGACRE ANDRE, SHIRLEY

APPLICANT: POTH, CHARLES

APPLICANT: NATO, EASIBABANG

APPLICANT: BARNWELL, JOHN

APPLICANT: MENDIS, FAMEE

TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF

FILE REFERENCE: ELITRA-011A

CURRENT FILING DATE: 1999-04-18

PATENT APPLICATION NUMBER: 09/134,333

FILE REFERENCE: 06/00135-0001P

CURRENT FILING DATE: 1999-04-18

PATENT APPLICATION NUMBER: 09/134,333

EARLIER FILING DATE: 1997-02-14

EARLIER APPLICATION NUMBER: FR96/01822

EARLIER FILING DATE: 1996-02-14

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 13

LENGTH: 380

TYPE: PRT

ORGANISM: Plasmodium vivax-like sp.

FEATURE:

OTHER INFORMATION: Amino Acids 1-140-REGION I

FEATURE:

OTHER INFORMATION: Amino Acids 141-174-REGION II

FEATURE:

OTHER INFORMATION: Amino Acids 175-293-PROION III

FEATURE:

OTHER INFORMATION: Amino Acids 294-300-REGION IV

FEATURE:

OTHER INFORMATION: Amino Acids 320-333-13

US-09-134-333-13

Query Match 11.68; Score 72; DB 10; Length 380;

Best local similarity 24.48; Prod No. 5.2; Mismatches 57; Indels 38; Gaps 6;

Matches 30; Conservative 26; Mismatches 57; Indels 38; Gaps 6;

QY 9 EVATLAWTVSGGVVZVYVQVETHTLMESVDEQVVFSLALVYLQVPEQV 60

Db 26 VLVTLACWHTVTVVQVQVAVTNTVQVQVQVQVQVQVQVQVQVQVQV 87

QY 51 EFTVY.....EMFTVAVMTTITM..... 33

Db 98 IIRTVVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 147

QY 32 MCEVTVVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 132

Db 149 VVTVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 184

RESULT 11

US-10-071-751-10

Sequence 39, Application US/10071751

Patent No. US20020149352A1

GENERAL INFORMATION:

APPLICANT: Hunter, Shirley Wu

Webster, Eric R.

TITLE OF INVENTION: NOVEL ENTEROPASITE SALIVA PROTEINS AND

APPARATUS TO COLLECT SUCH PROTEINS

NUMBER OF SEQUENCES: 99

CORRESPONDENCE ADDRESS:

APPROPRIATE: SHEPPARD PASS P.C.

STREET: 1560 BROADWAY, SUITE 1200

CITY: DENVER

STATE: CO

COUNTRY: U.S.A.

ZIP: 80202

COMPUTER FEATURES FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1 0. Version #1 30

CURRENT APPLICATION DATA: US/10/071,751

APPLICATION NUMBER: US/10/071,751

FILING DATE: 07 Feb 2002

CLASSIFICATION: <Unknown>

Prior APPLICATION DATA:

APPLICATION NUMBER: 09/171,156

FILING DATE: 1998-10-09

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Gary J.

PERCENTAGE NUMBER: 32,000

PRIOR APPLICATION NUMBER: 2618-17-04-PUS

TELEPHONE: 303/863-9700

TELEFAX: 303/863-9703


```

1 INFORMATION FOR SEQ ID NO: 30:
2
3 SEQUENCE CHARACTERISTICS:
4     LENGTH: 586 amino acids
5     TYPE: amino acid
6     TOPOLOGY: linear
7
8 MOLECULE TYPE: protein
9
10 FEATURE:
11     NAME/KEY: var_30
12     LOCATION: 179
13
14 SEQUENCE DESCRIPTION: SEQ
15
16 US 10 071 751 30

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[illegible]

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1  RESULT 12
2  US 09-870-759-86
3  : Sequence No. Application No. 09-870-759-86
4  : Patent No. US20020177551A1
5  : GENERAL INFORMATION
6  :
7  : APPLICANT: TERMAN, David S
8  : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEURONAL DYSFUNCTION
9  : FILE REFERENCE: 970759
10 :
11 : CURRENT APPLICATION NUMBER: US/09/470,744
12 : CURRENT FILING DATE: 2002-01-14
13 : PRIOR APPLICATION NUMBER: US 60/208,128
14 : PRIOR FILING DATE: 2000-05-30
15 : NUMBER OF SEQ. ID NOS.: 152
16 : SOFTWARE: Patent version 3.1
17 : SEQ ID NO 86
18 :
19 : LENGTH: 715
20 : TYPE: PRT
21 :
22 : ORGANISM: Staphylococcus aureus
23 : US 09 870-759-86

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Query Maltb. 1124, S. P. 34 7, DB 3, Torgel 715,
Best Local Similarity 1300, Tref 30,
Marches 11, Conservative 12, Mismatches 46, Indels 63, Gaps 7,
QY 9 VAILAMTVSGE-----DQKRYQVNEFFPLMPLHRLPQRLALPVLQELIN-----S
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 ITICGALVASSLFTWPAIVTQSPVNSPVNSKSTLTLSWYSGPTLESQF 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 -----HREPTETMTNIVAPMTTIAMTQVTVLQPLMKY-----96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 INAGILPILVYQPAVAGAMTP-----ILSHQVILKPAVYVGRKPKY 114
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 77 -----LRETNELNE KUFFTQISE-----KALPFFAPAV 114
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 QKVFNNPTSYGKLTQVQVQITFLTQPEVNETSLFGAVTQETIVETEN 168
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 13

US 09-881-752A-162

1. BACKGROUND: The Applicant is "752A-162A"

2. Patent No. US20030115078A1

3. GENERAL INFORMATION

4. APPLICANT: Kleinhous, Harold

5. APPLICANT: Al-Garawi, Amal

```

: APPLICANT: Miller, Charles
: APPLICANT: Tomb, Jean-Francois
: APPLICANT: Oomen, Raymond P.
: TITLE OF INVENTION: Identification of polynucleotides
: DATE OF INVENTION: Sep 11/94
: TITLE OF INVENTION: Genotype
: FILE REFERENCE: 06132/041002
: CURRENT APPLICATION NUMBER: US/09/881,752A
: CURRENT FILING DATE: 2001-06-15
: PRIOR APPLICATION NUMBER: US 08/833,457
: PRIOR FILING DATE: 1997-04-01
: NUMBER OF SEQ ID NOS: 370
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 162
: LENGTH: 228
: TYPE: PR1
: ORGANISM: Helicobacter pylori
: US 09/881,752A.162

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[illegible]

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RESULT 14
US-09-919-172-29
? ? ? ? ?
? Sequence CO Application No/08919172
? Patent No. US20020119463A1
? GENERAL INFORMATION:
? APPLICANT: Paris, Mary
? APPLICANT: Turck, Christopher M.
? TITLE OF INVENTION: PRESTATE DANCEP MAPKERS
? FILE REFERENCE: PA-0036 US
? CURRENT APPLICATION NUMBER: 03/06,919,172
? FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/223,469
? PRIOR FILING DATE: 2000-07-29
? NUMBER OF SEQ ID NOS.: 102
? SOFTWARE: PERL Program
? SEQ ID NO. 29
? LENGTH: 2125
? TYPE: PKT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? OTHER INFORMATION: If you find other information
US-09-919-172-29

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Query Match      11.0%; Score 73; DB 10; Length 2125;
Best Local Similarity 23.5%; Pred. No. 1.1e+02;
Matches 31; Conservative 24; Mismatches 47; Indels 30; Gaps 5;
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TYPE: amino acid
TOPOLOGY: linear
MOLFORM TYPE: protein
US 09 533-306A-4

Query Match 11.9%; Score 79; DB 2; Length 885;
Best Local Similarity 25.8%; Pred. No. 2.6;
Matches 31; Conservative 28; Mismatches 47; Indels 20; Gaps 7;

QY 3 VALLAVNVEGDAFQVYNEFFFLMPRIHEIKFDELALFYLDQINFFSEYPT---- 64
DB 313 ISLNIJUNFFFLFAS TVEAEKAPFFFLFPLTQ YEEFAANYK 364

QY 65 KEMFPTVAPMTTAMIVSVESVLEPL MFFQVQVPEVHEMFFVFFVTHLEPFL 100
DB 365 LKTFPHLLELLAVVLEINLQVLSVLEFFFLFLLAEENL ELAL ELAL 160

QY 121 KFEAEVY 129
DB 421 AEAEAREK 428

RESULT 5

US-08-742-923A-4

Sequence 4, Application 00/58742923A

Patent No. 5869611

GENERAL INFORMATION:

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APPLICANT: Collins, Francis S.

APPLICANT: Siciliano, Michael J.

APPLICANT: Claxton, David

TITLE OF INVENTION: Methods for Derivation of Peptides

TITLE OF INVENTION: Rearrangements

NUMBER OF SEQUENCES: 14

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STATE: MI

COUNTRY: USA

ZIP: 48303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/742,923A

FILING DATE: No. 5869611 member 1, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Smith, DeAnn F.

REGISTRATION NUMBER: 36683

REFERENCE/FILE NUMBER: 2115-0004-4109

TELECOMMUNICATION INFORMATION:

TELEPHONE: (810) 641-1600

TELEFAX: (810) 641-0270

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 885 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US 08-742-923A-4

Query Match 11.9%; Score 79; DB 2; Length 885;
Best Local Similarity 25.8%; Pred. No. 2.6;
Matches 31; Conservative 28; Mismatches 47; Indels 20; Gaps 7;

QY 3 VALLAVNVEGDAFQVYNEFFFLMPRIHEIKFDELALFYLDQINFFSEYPT 64
DB 313 ISLNIJUNFFFLFAS TVEAEKAPFFFLFPLTQ YEEFAANYK 364

QY 65 KEMFPTVAPMTTAMIVSVESVLEPL MFFQVQVPEVHEMFFVFFVTHLEPFL 120
DB 365 LKTFPHLLELLAVVLEINLQVLSVLEFFFLFLLAEENL ELAL ELAL 160

QY 121 KFEAEVY 128
DB 421 AEAEAREK 428

RESULT 6

5210183-2

Patent No. 5210183

APPLICANT: LINDAHL, GUNNAR FRITZ, ELISABET HELEN, LARS OLOF

TITLE OF INVENTION: PROTEIN ANT. WITH IMMUNOGLOBULIN A

BINDING ACTIVITY, THE CORRESPONDING VECTORS AND REAGENTS, REAGENT

ANT. AND PHARMACEUTICAL COMPOSITION

NUMBER OF SEQUENCES: 3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/270,099

FILING DATE: 14-NOV-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 186,097

FILING DATE: 25-APR-1988

SEQ ID NO: 2:

LENGTH: 344

5210183-2

Query Match 11.5%; Score 76.5; DB 6; Length 144;

Best Local Similarity 25.0%; Pred. No. 1.4;

Matches 31; Conservative 27; Mismatches 51; Indels 15; Gaps 5;

QY 11 PHQVQVHEPHTMPTMPSVPADELALFYLDQINFFSEYPTMEL KVAEMGILL 79
DB 102 PEQVQVHEPHTMPTMPSVPADELALFYLDQINFFSEYPTMEL KVAEMGILL 161

QY 90 AMIDVQVHEPHTMPTMPSVPADELALFYLDQINFFSEYPTMEL KVAEMGILL 129
DB 162 KQVQVHEPHTMPTMPSVPADELALFYLDQINFFSEYPTMEL KVAEMGILL 220

QY 128 KNEE 131
DB 221 KNEE 224

RESULT 7

5210183-3

Patent No. 5210183

APPLICANT: LINDAHL, GUNNAR FRITZ, ELISABET HELEN, LARS OLOF

TITLE OF INVENTION: PROTEIN ANT. WITH IMMUNOGLOBULIN A

BINDING ACTIVITY, THE CORRESPONDING VECTORS AND REAGENTS, REAGENT

ANT. AND PHARMACEUTICAL COMPOSITION

NUMBER OF SEQUENCES: 3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/270,099

FILING DATE: 14-NOV-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 186,097

FILING DATE: 25-APR-1988

SEQ ID NO: 3:

LENGTH: 683

5210183-3

Query Match 11.5%; Score 76.5; DB 6; Length 683;
Best Local Similarity 25.0%; Pred. No. 3.5;

Matches 31; Conservative 27; Mismatches 51; Indels 15; Gaps 5;

QY 11 PHQVQVHEPHTMPTMPSVPADELALFYLDQINFFSEYPTMEL KVAEMGILL 79
DB 102 PEQVQVHEPHTMPTMPSVPADELALFYLDQINFFSEYPTMEL KVAEMGILL 161

QY 90 AMIDVQVHEPHTMPTMPSVPADELALFYLDQINFFSEYPTMEL KVAEMGILL 129
DB 162 KQVQVHEPHTMPTMPSVPADELALFYLDQINFFSEYPTMEL KVAEMGILL 220


```

1 TYPE: amino acid
2 STRANDEDNESS: single
3 Tertiary structure
4 MOLECULE TYPE: protein
5 FEATURE:
6 NAME/KEY: K112
7 LOCATION: 1-496
8 OTHER INFORMATION: human TIE 2 ligand 2
9 US-08 740 223A 16

Query Match 11.18, Score 73.5, EE 4, Length 496
Best Local Similarity 20.38, Pred No. 4.9,
Matches 25, Conservative 26, Mismatches 37, Indels 35, Gaps 34

QV 37 RHHEHGHGKALSVLQCI 100
DB 155 RHHEHGHGKALSVLQCI 100
QV 41 RHHEHGHGKALSVLQCI 100
DB 215 RHHEHGHGKALSVLQCI 100
QV 122 KEE 124
DB 275 KEE 277

RESULT 13
US-09-709-189-16
1 Sequence 16, Application us/09709100
2 Patent No. 6245335
3 GENERAL INFORMATION:
4 APPLICANT: Masure, H. Robert
5 APPLICANT: Tuomanen, Elaine
6 APPLICANT: Tuomanen, Theresa M.
7 TITLE OF INVENTION: NOVEL HUMAN TIE 2 LIGAND
8 NUMBER OF SEQUENCES: 25
9 CORRESPONDENCE ADDRESS:
10 ADDRESS: David A. Jackson, Ph.D.
11 STREET: 411 Hawthorne Ave., Continental Plaza, 4th
12 CITY: Hackensack
13 STATE: NJ 07601-1001
14 COUNTRY: USA
15 ZIP: 07601-1001
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC DOS/MS DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.0
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: 09/042,473
23 FILING DATE: 16-OCT-1997
24 PRIORITY DATE: 18-FEB-1997
25 APPLICATION NUMBER: 09/029,444
26 FILING DATE: 18-FEB-1997
27 PRIORITY DATE: 19-SEP-1997
28 APPLICATION NUMBER: 09/059,368
29 FILING DATE: 16-OCT-1997
30 APPLICATION NUMBER: 09/042,473
31 ATTORNEY/AGENT INFORMATION:
32 NAME: MUSTING, Ann M.
33 PARTICIPATION NUMBER: 33,977
34 REFERENCE/AGENT NUMBER: 119 00430101
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 612 305-1217
37 TELEFAX: 612 305-1228
38 INFORMATION FOR SEQ ID NO: 6:
39 FEATURE MAP:
40 LENGTH: 564 amino acids
41 TYPE: amino acid
42 STRANDEDNESS: single
43 Tertiary structure
44 MOLECULE TYPE: protein
45 US-09-305 025 6

Query Match 11.08, Score 73.5, EE 4, Length 564
Best Local Similarity 20.38, Pred No. 4.9,
Matches 25, Conservative 26, Mismatches 37, Indels 35, Gaps 34

QV 37 RHHEHGHGKALSVLQCI 100
DB 155 RHHEHGHGKALSVLQCI 100
QV 41 RHHEHGHGKALSVLQCI 100
DB 215 RHHEHGHGKALSVLQCI 100
QV 122 KEE 124
DB 275 KEE 277

RESULT 14
US-09-709-189-16
1 Sequence 16, Application us/09709100
2 Patent No. 6245335
3 GENERAL INFORMATION:
4 APPLICANT: Masure, H. Robert
5 APPLICANT: Tuomanen, Elaine
6 APPLICANT: Tuomanen, Theresa M.
7 TITLE OF INVENTION: NOVEL HUMAN TIE 2 LIGAND
8 NUMBER OF SEQUENCES: 25
9 CORRESPONDENCE ADDRESS:
10 ADDRESS: David A. Jackson, Ph.D.
11 STREET: 411 Hawthorne Ave., Continental Plaza, 4th
12 CITY: Hackensack
13 STATE: NJ 07601-1001
14 COUNTRY: USA
15 ZIP: 07601-1001
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC DOS/MS DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.0
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: 09/042,473
23 FILING DATE: 16-OCT-1997
24 PRIORITY DATE: 18-FEB-1997
25 APPLICATION NUMBER: 09/029,444
26 FILING DATE: 18-FEB-1997
27 PRIORITY DATE: 19-SEP-1997
28 APPLICATION NUMBER: 09/059,368
29 FILING DATE: 16-OCT-1997
30 APPLICATION NUMBER: 09/042,473
31 ATTORNEY/AGENT INFORMATION:
32 NAME: MUSTING, Ann M.
33 PARTICIPATION NUMBER: 33,977
34 REFERENCE/AGENT NUMBER: 119 00430101
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 612 305-1217
37 TELEFAX: 612 305-1228
38 INFORMATION FOR SEQ ID NO: 6:
39 FEATURE MAP:
40 LENGTH: 564 amino acids
41 TYPE: amino acid
42 STRANDEDNESS: single
43 Tertiary structure
44 MOLECULE TYPE: protein
45 US-09-305 025 6

```

```

CORRESPONDENCE ADDRESS:
1 ADDRESS: MUSTING, Ann M.
2 STREET: 411 Hawthorne Ave., Continental Plaza, 4th
3 CITY: Hackensack
4 STATE: NJ 07601-1001
5 COUNTRY: USA
6 ZIP: 07601-1001
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC DOS/MS DOS
11 SOFTWARE: Patent In Release #1.0, Version #1.0
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: 09/042,473
14 FILING DATE: 16-OCT-1997
15 PRIORITY DATE: 18-FEB-1997
16 APPLICATION NUMBER: 09/029,444
17 FILING DATE: 18-FEB-1997
18 PRIORITY DATE: 19-SEP-1997
19 APPLICATION NUMBER: 09/059,368
20 FILING DATE: 16-OCT-1997
21 APPLICATION NUMBER: 09/042,473
22 ATTORNEY/AGENT INFORMATION:
23 NAME: MUSTING, Ann M.
24 PARTICIPATION NUMBER: 33,977
25 REFERENCE/AGENT NUMBER: 119 00430101
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 612 305-1217
28 TELEFAX: 612 305-1228
29 INFORMATION FOR SEQ ID NO: 6:
30 FEATURE MAP:
31 LENGTH: 564 amino acids
32 TYPE: amino acid
33 STRANDEDNESS: single
34 Tertiary structure
35 MOLECULE TYPE: protein
36 US-09-305 025 6

Query Match 11.08, Score 73.5, EE 4, Length 564
Best Local Similarity 20.38, Pred No. 4.9,
Matches 25, Conservative 26, Mismatches 37, Indels 35, Gaps 34

QV 37 RHHEHGHGKALSVLQCI 100
DB 155 RHHEHGHGKALSVLQCI 100
QV 41 RHHEHGHGKALSVLQCI 100
DB 215 RHHEHGHGKALSVLQCI 100
QV 122 KEE 124
DB 275 KEE 277

RESULT 15
US-09-709-189-16
1 Sequence 25, Application US/09847065
2 Patent No. 6245335
3 GENERAL INFORMATION:
4 APPLICANT: Masure, H. Robert
5 APPLICANT: Rosenow, Carsten I.
6 APPLICANT: Tuomanen, Elaine
7 APPLICANT: Tuomanen, Theresa M.
8 TITLE OF INVENTION: NOVEL HUMAN TIE 2 LIGAND
9 NUMBER OF SEQUENCES: 25
10 CORRESPONDENCE ADDRESS:
11 ADDRESS: David A. Jackson, Ph.D.
12 STREET: 411 Hawthorne Ave., Continental Plaza, 4th
13 CITY: Hackensack
14 STATE: NJ 07601-1001
15 COUNTRY: USA
16 ZIP: 07601-1001
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC DOS/MS DOS
21 SOFTWARE: Patent In Release #1.0, Version #1.0
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: 09/042,473
24 FILING DATE: 16-OCT-1997
25 PRIORITY DATE: 18-FEB-1997
26 APPLICATION NUMBER: 09/029,444
27 FILING DATE: 18-FEB-1997
28 PRIORITY DATE: 19-SEP-1997
29 APPLICATION NUMBER: 09/059,368
30 FILING DATE: 16-OCT-1997
31 APPLICATION NUMBER: 09/042,473
32 ATTORNEY/AGENT INFORMATION:
33 NAME: MUSTING, Ann M.
34 PARTICIPATION NUMBER: 33,977
35 REFERENCE/AGENT NUMBER: 119 00430101
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: 612 305-1217
38 TELEFAX: 612 305-1228
39 INFORMATION FOR SEQ ID NO: 6:
40 FEATURE MAP:
41 LENGTH: 564 amino acids
42 TYPE: amino acid
43 STRANDEDNESS: single
44 Tertiary structure
45 MOLECULE TYPE: protein
46 US-09-305 025 6

```



```

: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-POS/MS-POS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/847,065
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 36,742
: REFERENCE/DOCKET NUMBER: 600-1-158 ..
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 631 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEetical: NO
: FRAGMENT TYPE: N-terminal
: US-08 847-065-25

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Query Match      11.0%; Score 73; DB 4; Length 631;
Best Local Similarity 27.0%; Pred. No. 7.5;
Matches 27; Conservative 12; Mismatched 33; Indels 28; Gaps 3;

QY 14 LMERHEDQ-----IKKGFALFVLQRIHFFSEKPKYKIVAFMDTIAMIDGVPV 98
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 7 LDRKHTGNVALNKLKSAIKYVLPK-LNVLEKSKDELSPSEIKVLDL----- 54

QY 89 LDRLMQPKDIDIFCYNIEMFMFNSGDILEPTLYPEAPVY 128
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 55 -----AFKKFKDTLKPKGVAAKAKKVEEAKKK 83

```

```

Search completed: March 12, 2003, 13:27:22
Job time : 21.1211 secs

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The first part of the paper discusses the importance of understanding the cultural context of the research. It highlights the need for researchers to be sensitive to the values and beliefs of the communities they are studying. This is particularly important in the field of education, where cultural differences can significantly impact learning outcomes.

The second part of the paper focuses on the methodology used in the study. It describes the process of selecting participants, collecting data, and analyzing the results. The authors emphasize the importance of using a mixed-methods approach, which allows for a more comprehensive understanding of the research topic.

The third part of the paper presents the findings of the study. It discusses the results of the quantitative data analysis and the insights gained from the qualitative interviews. The authors conclude that there are significant differences in learning outcomes between different cultural groups, and these differences can be attributed to a variety of factors, including language barriers and cultural differences in learning styles.

The final part of the paper discusses the implications of the findings for future research and practice. It suggests that educators should be aware of the cultural differences in their classrooms and develop strategies to support all learners. Additionally, it recommends that future research should continue to explore the cultural factors that influence learning outcomes.

GenCore version 5.1.4 p5 4578
Copyright (c) 1991-2003 J. Drenth Ltd.

OM protein: protein search, using sw model

Run on: March 12, 2003, 08:41:15, Search time for peak records
(without alignments)
605.14; Million cells updates/sec

Title: uc 09 877 160 2

Perfect score: 1689

Sequence: 1 MFTVLAIAACUACALCAVYAP.....VFAMHDLMMIEYVYVIL 323

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 56134422 residues

Total number of hits satisfying chosen parameters. 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Fast processing: Minimum Match 34
Maximum Match 1004
Listing first 45 summaries

Database: PIR 73.4

1: p1r1.4

2: p1r2.4

3: p1r3.4

4: p1r4.4

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1396.5	82.7	319	2	A61500
2	1251	74.1	245	2	allergen Der f 1 p
3	984.5	58.3	211	2	probable cysteine
4	387	22.9	336	2	cathepsin L-like p
5	385.5	22.8	94	2	major fecal allerg
6	380.5	22.5	148	2	probable cysteine
7	379.5	22.5	148	2	cathepsin L (EC 3.4.22
8	371.5	22.1	322	2	cysteine proteinase
9	371.5	22.0	324	2	cathepsin L (EC 3.4.22
10	368.5	21.5	342	2	cathepsin L-like p
11	367	21.7	326	2	cysteine proteinase
12	366.5	21.7	342	2	cysteine proteinase
13	363.5	21.5	454	2	JC4848
14	362.5	21.5	343	1	PEC
15	362.5	21.5	367	2	JN0634
16	362	21.4	323	2	J-7472
17	360	21.3	323	2	S19650
18	359.5	21.3	342	2	C96412
19	359.5	21.3	342	2	T09760
20	359.5	21.3	374	2	T03941
21	358	21.2	380	1	TAGB
22	355.5	21.1	341	2	T45839
23	355.5	21.0	349	2	T09798
24	355.5	21.0	368	2	S47312
25	355	21.0	337	2	T24387
26	354	21.0	359	2	JC7787
27	353	20.9	467	2	A46454
28	352.5	20.9	466	2	T06416
29	351.5	20.9	351	2	T10501

30 345 20.4 364 2 T12039
31 344 20.4 324 2 G62035
32 344 20.4 367 2 T04207
33 343.5 20.3 345 2 T07839
34 343 20.3 362 2 T08529
35 342.5 20.3 324 2 T05519
36 342.5 20.3 355 2 T06102
37 342 20.3 363 2 T07772
38 342.5 20.3 378 2 S47434
39 342 20.2 362 2 T05777
40 342 20.2 364 2 T06030
41 342.5 20.2 459 2 S07011
42 341 20.2 340 2 T10516
43 339.5 20.1 460 2 S41602
44 339 20.1 480 2 T01206
45 338.5 20.0 329 2 S74227

ALIGNMENTS

RESULT 1

A61500

allergen Der f 1 precursor house dust mite (Dermatophagoides farinae)

C:Species: Dermatophagoides farinae

C>Date: 97-Oct-1994 #sequence_revision 00001 114 #rev_date: 11 Aug 1999

C:Accession: A61500

R:Dilworth, R.J.; Chua, K.Y.; Thomas, W.R.

Clin. Exp. Allergy 21, 25-32, 1991

A:Title: Sequence analysis of cDNA coding for a major house dust mite allergen, Der f 1

A:Reference number: A61500; M01D:91215493; PMID:2021874

A:Accession: A61500

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-319 <DIL>

C:Superfamily: papain

Query Match 82.7%, Score 1396.5, DB 2, Length 319;

Best Local Similarity 82.2%, Pred. No. 1e-106;

Matches 264; Conservative 26; Mismatches 28; Indels 3; Gaps 3;

QY 1 MFTVLAIAACUACALCAVYAPSSIVTHERVPAFNSVAIFEEELBAPNHLSEVYVQSN 60
DB 1 MFTVLAIAACUACALCAVYAPSSIVTHERVPAFNSVAIFEEELBAPNHLSEVYVQSN 58
QY 61 GGAINHLSLSLEPTFRFMSAEAEHLETFDLMATNASSING NAPAETLEKQET 119
DE 59 KGAINHLSLSLEPTFRFVLSMAAEQLTFTLLMAETSACTHGVVTFSLISGLT 119
QY 120 VTPIRMGGGGSQWAFSSVANTESAVLAYNPSLLLAETELVTFASCHTCHETIFRGIE 179
DB 119 VTPIRMGGGGSQWAFSSVANTESAVLAYNPSLLLAETELVTFASCHTCHETIFRGIE 178
QY 180 YLCHHNVVLELYVEYVAPESGPPPHAFEPFIDNNVAVVPPVNVVIRKALAVHSALAVI 239
DB 179 YLCHHNVVLELYVEYVAPESGPPPHAFEPFIDNNVAVVPPVNVVIRKALAVHSALAVI 238
QY 240 ITHFDGAFPHDQFTTLLSGHNGAFPHVAVVAVVAVVAVVAVVAVVAVVAVVAVV 299
DB 239 ITHFDGAFPHDQFTTLLSGHNGAFPHVAVVAVVAVVAVVAVVAVVAVVAVVAVV 298
QY 300 GYFANIDLMWIEYVYVIL 300
DB 299 GYFAGNLMWIEYVYVIM 319

RESULT 2

J00337

allergen Der p 1 house dust mite (Dermatophagoides pteronyssinus) (fragment)

C:Species: Dermatophagoides pteronyssinus

C:Date: 07 Sep 1990 #sequence_revision 00001 114 #rev_date: 11 Aug 1999

C:Accession: J00337; A07582; A31657; C07634

R:Chua, K.Y.; Stewart, G.A.; Thomas, W.R.; Simpson, R.J.; Dilworth, R.J.; Piczka, T.M.

[illegible]

Y₁ Y₂ Y₃ Y₄ Y₅ Y₆ Y₇ Y₈ Y₉ Y₁₀ Y₁₁ Y₁₂ Y₁₃ Y₁₄ Y₁₅ Y₁₆ Y₁₇ Y₁₈ Y₁₉ Y₂₀ Y₂₁ Y₂₂ Y₂₃ Y₂₄ Y₂₅ Y₂₆ Y₂₇ Y₂₈ Y₂₉ Y₃₀ Y₃₁ Y₃₂ Y₃₃ Y₃₄ Y₃₅ Y₃₆ Y₃₇ Y₃₈ Y₃₉ Y₄₀ Y₄₁ Y₄₂ Y₄₃ Y₄₄ Y₄₅ Y₄₆ Y₄₇ Y₄₈ Y₄₉ Y₅₀ Y₅₁ Y₅₂ Y₅₃ Y₅₄ Y₅₅ Y₅₆ Y₅₇ Y₅₈ Y₅₉ Y₆₀ Y₆₁ Y₆₂ Y₆₃ Y₆₄ Y₆₅ Y₆₆ Y₆₇ Y₆₈ Y₆₉ Y₇₀ Y₇₁ Y₇₂ Y₇₃ Y₇₄ Y₇₅ Y₇₆ Y₇₇ Y₇₈ Y₇₉ Y₈₀ Y₈₁ Y₈₂ Y₈₃ Y₈₄ Y₈₅ Y₈₆ Y₈₇ Y₈₈ Y₈₉ Y₉₀ Y₉₁ Y₉₂ Y₉₃ Y₉₄ Y₉₅ Y₉₆ Y₉₇ Y₉₈ Y₉₉ Y₁₀₀ Y₁₀₁ Y₁₀₂ Y₁₀₃ Y₁₀₄ Y₁₀₅ Y₁₀₆ Y₁₀₇ Y₁₀₈ Y₁₀₉ Y₁₁₀ Y₁₁₁ Y₁₁₂ Y₁₁₃ Y₁₁₄ Y₁₁₅ Y₁₁₆ Y₁₁₇ Y₁₁₈ Y₁₁₉ Y₁₂₀ Y₁₂₁ Y₁₂₂ Y₁₂₃ Y₁₂₄ Y₁₂₅ Y₁₂₆ Y₁₂₇ Y₁₂₈ Y₁₂₉ Y₁₃₀ Y₁₃₁ Y₁₃₂ Y₁₃₃ Y₁₃₄ Y₁₃₅ Y₁₃₆ Y₁₃₇ Y₁₃₈ Y₁₃₉ Y₁₄₀ Y₁₄₁ Y₁₄₂ Y₁₄₃ Y₁₄₄ Y₁₄₅ Y₁₄₆ Y₁₄₇ Y₁₄₈ Y₁₄₉ Y₁₅₀ Y₁₅₁ Y₁₅₂ Y₁₅₃ Y₁₅₄ Y₁₅₅ Y₁₅₆ Y₁₅₇ Y₁₅₈ Y₁₅₉ Y₁₆₀ Y₁₆₁ Y₁₆₂ Y₁₆₃ Y₁₆₄ Y₁₆₅ Y₁₆₆ Y₁₆₇ Y₁₆₈ Y₁₆₉ Y₁₇₀ Y₁₇₁ Y₁₇₂ Y₁₇₃ Y₁₇₄ Y₁₇₅ Y₁₇₆ Y₁₇₇ Y₁₇₈ Y₁₇₉ Y₁₈₀ Y₁₈₁ Y₁₈₂ Y₁₈₃ Y₁₈₄ Y₁₈₅ Y₁₈₆ Y₁₈₇ Y₁₈₈ Y₁₈₉ Y₁₉₀ Y₁₉₁ Y₁₉₂ Y₁₉₃ Y₁₉₄ Y₁₉₅ Y₁₉₆ Y₁₉₇ Y₁₉₈ Y₁₉₉ Y₂₀₀ Y₂₀₁ Y₂₀₂ Y₂₀₃ Y₂₀₄ Y₂₀₅ Y₂₀₆ Y₂₀₇ Y₂₀₈ Y₂₀₉ Y₂₁₀ Y₂₁₁ Y₂₁₂ Y₂₁₃ Y₂₁₄ Y₂₁₅ Y₂₁₆ Y₂₁₇ Y₂₁₈ Y₂₁₉ Y₂₂₀ Y₂₂₁ Y₂₂₂ Y₂₂₃ Y₂₂₄ Y₂₂₅ Y₂₂₆ Y₂₂₇ Y₂₂₈ Y₂₂₉ Y₂₃₀ Y₂₃₁ Y₂₃₂ Y₂₃₃ Y₂₃₄ Y₂₃₅ Y₂₃₆ Y₂₃₇ Y₂₃₈ Y₂₃₉ Y₂₄₀ Y₂₄₁ Y₂₄₂ Y₂₄₃ Y₂₄₄ Y₂₄₅ Y₂₄₆ Y₂₄₇ Y₂₄₈ Y₂₄₉ Y₂₅₀ Y₂₅₁ Y₂₅₂ Y₂₅₃ Y₂₅₄ Y₂₅₅ Y₂₅₆ Y₂₅₇ Y₂₅₈ Y₂₅₉ Y₂₆₀ Y₂₆₁ Y₂₆₂ Y₂₆₃ Y₂₆₄ Y₂₆₅ Y₂₆₆ Y₂₆₇ Y₂₆₈ Y₂₆₉ Y₂₇₀ Y₂₇₁ Y₂₇₂ Y₂₇₃ Y₂₇₄ Y₂₇₅ Y₂₇₆ Y₂₇₇ Y₂₇₈ Y₂₇₉ Y₂₈₀ Y₂₈₁ Y₂₈₂ Y₂₈₃ Y₂₈₄ Y₂₈₅ Y₂₈₆ Y₂₈₇ Y₂₈₈ Y₂₈₉ Y₂₉₀ Y₂₉₁ Y₂₉₂ Y₂₉₃ Y₂₉₄ Y₂₉₅ Y₂₉₆ Y₂₉₇ Y₂₉₈ Y₂₉₉ Y₃₀₀ Y₃₀₁ Y₃₀₂ Y₃₀₃ Y₃₀₄ Y₃₀₅ Y₃₀₆ Y₃₀₇ Y₃₀₈ Y₃₀₉ Y₃₁₀ Y₃₁₁ Y₃₁₂ Y₃₁₃ Y₃₁₄ Y₃₁₅ Y₃₁₆ Y₃₁₇ Y₃₁₈ Y₃₁₉ Y₃₂₀ Y₃₂₁ Y₃₂₂ Y₃₂₃ Y₃₂₄ Y₃₂₅ Y₃₂₆ Y₃₂₇ Y₃₂₈ Y₃₂₉ Y₃₃₀ Y₃₃₁ Y₃₃₂ Y₃₃₃ Y₃₃₄ Y₃₃₅ Y₃₃₆ Y₃₃₇ Y₃₃₈ Y₃₃₉ Y₃₄₀ Y₃₄₁ Y₃₄₂ Y₃₄₃ Y₃₄₄ Y₃₄₅ Y₃₄₆ Y₃₄₇ Y₃₄₈ Y₃₄₉ Y₃₅₀ Y₃₅₁ Y₃₅₂ Y₃₅₃ Y₃₅₄ Y₃₅₅ Y₃₅₆ Y₃₅₇ Y₃₅₈ Y₃₅₉ Y₃₆₀ Y₃₆₁ Y₃₆₂ Y₃₆₃ Y₃₆₄ Y₃₆₅ Y₃₆₆ Y₃₆₇ Y₃₆₈ Y₃₆₉ Y₃₇₀ Y₃₇₁ Y₃₇₂ Y₃₇₃ Y₃₇₄ Y₃₇₅ Y₃₇₆ Y₃₇₇ Y₃₇₈ Y₃₇₉ Y₃₈₀ Y₃₈₁ Y₃₈₂ Y₃₈₃ Y₃₈₄ Y₃₈₅ Y₃₈₆ Y₃₈₇ Y₃₈₈ Y₃₈₉ Y₃₉₀ Y₃₉₁ Y₃₉₂ Y₃₉₃ Y₃₉₄ Y₃₉₅ Y₃₉₆ Y₃₉₇ Y₃₉₈ Y₃₉₉ Y₄₀₀ Y₄₀₁ Y₄₀₂ Y₄₀₃ Y₄₀₄ Y₄₀₅ Y₄₀₆ Y₄₀₇ Y₄₀₈ Y₄₀₉ Y₄₁₀ Y₄₁₁ Y₄₁₂ Y₄₁₃ Y₄₁₄ Y₄₁₅ Y₄₁₆ Y₄₁₇ Y₄₁₈ Y₄₁₉ Y₄₂₀ Y<

GenCore version 5.1.4 rev 4747
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OM protein - protein search, using sw model

Run on: March 12, 2003, 08:22:06 Search time: 1700 seconds
(without alignments)
926.437 Million cell updates/sec

Title: US-09-877-160-2

Perfect score: 1689

Sequence: 1 MKIVLAFASILLASVAYSP.....YFANNIDLMWIEEYFVWIL 320

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Scanned: 671580 seqs, 265047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 6

Maximum seq length: 320

Post processing: Minimum Match 98

Maximum Match 100

Listing first 45 summaries

Database:

SPTREMBL 21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_protist:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacterioph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	953.5	56.5	210	5	Q95X05	Q95X05 dermatophag
2	616	36.5	146	5	Q95X05	Q95X05 dermatophag
3	473	28.0	107	5	Q95X04	Q95X04 dermatophag
4	445	26.3	133	5	Q968Y3	Q968Y3 dermatophag
5	392.5	23.2	445	10	Q968Y2	Q968Y2 dermatophag
6	389.5	23.2	326	10	Q968Y2	Q968Y2 dermatophag
7	387	22.9	326	5	Q968Y2	Q968Y2 dermatophag
8	386	22.9	326	5	Q968Y2	Q968Y2 dermatophag
9	381	22.6	324	5	Q97397	Q97397 phage
10	380.5	22.5	346	10	Q95CH7	Q95CH7 arabidopsis
11	380	22.5	324	5	Q8T0X0	Q8T0X0 fasciola he
12	378	22.4	461	10	Q95X05	Q95X05 dermatophag
13	375	22.2	311	5	Q968W6	Q968W6 fasciola he
14	374	22.1	321	5	Q968Y4	Q968Y4 fasciola he
15	374	22.1	326	5	Q968W4	Q968W4 fasciola he
16	371	22.1	326	5	Q968Y4	Q968Y4 fasciola he

17	370.5	21.9	326	5	Q968W3	Q968W3 fasciola he
18	368	21.8	326	5	Q968Y2	Q968Y2 fasciola he
19	367.5	21.8	326	5	Q968Y4	Q968Y4 fasciola he
20	367	21.7	326	5	Q24540	Q24540 fasciola he
21	366.5	21.7	342	10	Q41721	Q41721 zinnia eleg
22	366	21.7	324	5	Q97392	Q97392 hypera post
23	365	21.6	306	5	Q968W4	Q968W4 fasciola he
24	364.5	21.6	324	10	Q968Y4	Q968Y4 fasciola he
25	364.5	21.6	326	5	Q24941	Q24941 fasciola he
26	364.5	21.6	326	5	Q95NFI	Q95NFI spirochaeta
27	364.5	21.6	326	5	Q95NFI	Q95NFI spirochaeta
28	364	21.6	311	5	Q968W5	Q968W5 fasciola he
29	363.5	21.5	454	10	Q43922	Q43922 fasciola he
30	363	21.5	310	5	Q96710	Q96710 fasciola he
31	362.5	21.5	367	10	Q43923	Q43923 fasciola he
32	362.5	21.5	443	5	Q968Y2	Q968Y2 fasciola he
33	362.5	21.5	443	5	Q968Y2	Q968Y2 fasciola he
34	361.5	21.4	375	5	Q968Y2	Q968Y2 fasciola he
35	361	21.4	381	5	Q968Y2	Q968Y2 fasciola he
36	360	21.3	316	5	Q968Y2	Q968Y2 fasciola he
37	359.5	21.3	322	5	Q968Y2	Q968Y2 fasciola he
38	359.5	21.3	346	10	Q968Y2	Q968Y2 fasciola he
39	359.5	21.3	374	10	Q968Y2	Q968Y2 fasciola he
40	359.5	21.3	374	10	Q968Y2	Q968Y2 fasciola he
41	359	21.3	380	10	Q968Y2	Q968Y2 fasciola he
42	358.5	21.2	324	10	Q968Y2	Q968Y2 fasciola he
43	358.5	21.2	329	10	Q968Y2	Q968Y2 fasciola he
44	358	21.2	390	10	Q968Y2	Q968Y2 fasciola he
45	357	21.1	311	5	Q968Y2	Q968Y2 fasciola he

ALIGNMENTS

RESULT 1

Q9GY0
ID Q9GY0 PRELIMINARY: PPT: 210 AA.
AC Q9GY0
DT 01-MAR-2001 (Trembl, 16, Created)
DT 01-MAR-2001 (Trembl, 16, Last sequence update)
DT 01-MAR-2001 (Trembl, 16, Last annotation update)
DE Allergen Der fl (Fragment)
OS Dermatophagoides farinae (House-dust mite).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcophagales; Acarididae; Analgoidea; Pyroglyphidae;
OC Dermatophagoides.
OX NCBI_TaxID=6954;
RN [1]
RP SEQUENCE FROM N.A.
FA Hae M.T., Xu J., Zhong H.G.;
FT "Cloning and sequencing of Der fl cDNA from Dermatophagoides
RT farinae."
RL Submitted (JUL-2000) to the EMBL/GenBank/EBI databases.
FM PI: AF285763; AAC00520.1;
DR HSP: P07688; IQDQ.
DR MEADS; C01075;
DE InterPro: IPR000668; Peptidase_C1.
DE InterPro: IPR000668; SHPOT acsite.
DR Pfam: PF00112; Peptidase_C17.1.
DR PRINTS: PR00705; PAPAIN_
DR ProDom: PD000158; Peptidase_C17.1.
DR PROSITE: PS00640; THIOLESTERASE_ACH, 1.
DR PROSITE: PS00640; THIOLESTERASE_ACH, 1.
DR PROSITE: PS00640; THIOLESTERASE_ACH, 1.
FT NON TER 1 1
FT NON TER 210 210
SQ SEQUENCE 210 AA, 3545 MW, EAc00520.1:EE59 CR64;

Query Match: 56.5%; Score 953.5, E6.5, Length 210;
Best Local Similarity: 92.4%; Pred. No. 1.5e-73;
Matches: 173, Conservative: 15, Mismatches: 11, Indels: 1, Gaps: 1;
29 100 MATCHING UNFAVORABLE, 95% IDENTICAL, 100% IDENTICAL, 100%

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Query Match      36.5%  Score 616;  DB 5;  Length 146;
Best Local Similarity  85.7%  Pred. No. 6.1e-45;
Matches 114;  Conservative  8;  Mismatches 11;  Indels  0;  Gaps
                                .
QY  137  CVAATETAYLAVERSSILAFPHIVTASCHWCHWERTTFRFVYIQRKGVQVQSSYVYVVA 146
DB  1  EVAAETAYLAIVPTLQVQVPELVKVVVQASGDSYHIVTFRFVYIQRKGVQVQSSYVYVVA 4
QY  137  RQCEPRRPHAPRFGISGVQVYVNNVKKREALACTHCAIATVQVETLQAPHHQCPET 356
DB  1  RALALPRNSMGLLENVLEVVHTEVYVKEALCTHCAIATVQVETLQAPHHQCPET 356
QY  257  IQRNGYGVNVHA 269
DB  121  IQRNGYGVNVHA 133
                                .
RESULT 3
CRIM4
ID  Q95X04  PRELIMINARY;  PRT;  107 AA.
AC  Q95X04.
DT  01-DEC-2001 (TRENBLrel. 19, Created)
DT  01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT  01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE  Cysteine proteinase (Fragment)
GN  CPW3
OS  Dermatophagoides farinac (House-dust mite).
RA  Yajima; Maraca; Arthropoda; Chelicerata; Arachnida; Acari;
OC  Acariformes, Sarcoptiformes; Astigmata; Pyroglyphidae;
OC  Dermatophagoides.

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OX NCBI_TaxID=6954;
RN [1]
RP SEQUENCE FROM N.A..
PP Park H , Yun H Y , Kim K Y , Park S Y , Yun H C.;
PT "Dermatophagoides farinae cysteine proteinase (PCPW) mRNA";
FL Submitted (JUL-1998) to the EMBL GenBank/GenPe databases.
DR EMBL; AF194432; AAL14425.1; -;
CP InterPro; IPR000687; Peptidase_C1.
CC InterPro; IPF000169; SHprot_acsite.
PF Pfam; PF00112; Peptide_C1; 1.
CD ProDom; PD000158; Peptide_C1; 1.
CE PROSITE; PS00639; THIO_PROTEASE_HIS; UNPROOWN_1.
CF NON TER
FT FTNONTER      1       107
SQ SEQUENCE     107 AA; 12277 MW; ASQETSTGSCAGFSQA CPCG4;

Query Match          28.0%; Score 473; DB 5; Length 107;
Best Local Similarity    21.3%; Pred.No. 6.6e-33;
Matches   87, Conservative        8; Mismatches 10; Indels 0; Gaps 0

2y 175 PGGHVVTHGVNVAVERVTVHPWSPKSGTTPRHHQPSFGYGVVGYFYHWPKVPALADOMVS QSA
DP : PGSHVEVDGVWEESNVDAASPEEAEFEFFPHTVTQTNTGTTFPHVFCTFHFPGLPGTTTG
CV 235 ATAVITIVTCIAAPRRVCSEDTICATPVNAIENHNAAIVMAACQC T81
DB 51 ATAVITHIHAFQHVNDSIFHFCHFNPDENVMMANVVGNGTGV V97

RESULT 4
O96B8Y3 PRELIMINARY; PROT; 133 AA.
ID IC O96BY3;
DC O1-PKC-2001 /T-EMBLrel 19, Created)
DT O1-PKC-2001 /T-EMBLrel 19, Last sequence update)
DD O1-MAR-2002 /T-EMBLrel 20, Last annotation update)
DE Cysteine proteinase (Fragment).
OC Peritrichalides pteromyximus (House-dust mite),
OC Fukuyuta; Metazoa; Artirogoda; Chelicerata; Arachnida; Acari;
OC acariformes, Sarcoptiformes, Astigmata; Analgoidea; Pyroglyphidae;
OC Dermatophagoides.
CX NCBI_TaxId=6954;
RN [1]
RP SEQUENCE FROM N.A..
PP Park H , Yun H Y , Kim K Y , Park S Y , Park S K.;
PT "Dermatophagoides pteronyssinus cysteine proteinase (Cpw1) mRNA.";
FL Submitted (APP-1998) to the EMBL/GenBank/GenPe database.
DR EMBL; AF145247; AK39773.1; -;
CP InterPro; IPR000689; Peptidase_C1.
CC InterPro; IPF000689; Peptidase_C1; 1.
PF Pfam; PF00112; Peptide_C1; 1.
CD ProDom; PD000159; Peptide_C1; 1.
CE NON TPP      1       1
CF NON TER      133      133
SQ SEQUENCE    133 AA; 14955 MW; FLLMDFPIELVFAQP CPCG4;

Query Match          26.3%; Score 445; DB 5; Length 133;
Best Local Similarity    20.1%; Pred.No. 2.e-30;
Matches   62, Conservative       19; Mismatches 10; Indels 0; Gaps 0

QY 129 CSSEMTSSGAATGSAYLVNFSDTAAPTLVTSACDGNSMPRTIFFSPLLTGRNQTO L88
DL 1 CGSWAPAFAQNASAVAPFDGINLADELVLCAAPPOHCQTIPPGIPLYCGNCIVE 60

CY 149 ENPHTVANLSCTHFNAAFEPHSHTLIHQSNQPTFRSLACTGFANTTIPTLPRAF Q48
DL 61 EGAMERAKRMKELEPNESHSEQCSHEKNELLIALTKEDADVGMNNHRPAF LCO

CY 242 PHYGGETTIQQP D60
DB 121 PHYQSQVIITD 132

RESULT 5
```

Q95VA7 PRELIMINARY; PRT; 445 AA.
 AC Q95VA7
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Consensus associated tyrosine protease (Fragm)
 GN CPT.
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eucomidiales; core eudicotyledons; Eridaceae;
 OC eurosidia II; Brassicales; Brassicaceae; Praecoxeae; Praecoxeae;
 GN CPT.
 [1]
 SEQUENCE FROM N.A.
 RA Coupe S.A., Sinclair B.K., Watson I.M., Pason J.R.,
 RT "Cysteine proteases and trypsin-like enzymes: cloning, characterization
 RT and contribution to the protease",
 RL Submitted (SEP 2001) to the FWP/GenBank/TrEMBL databases.
 DR EMBL; AF454956; AAL60578.1;
 DR InterPro; IPR000118; Granulin
 DR InterPro; IPR000648; Peptidase_C1
 DR InterPro; IPR000169; Suppt_actin
 DR Pfam; PF00396; granulin_1
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR PRINTS; PR00705; PAPAIN
 DR ProDom; PD00154; Peptidase_C1; 1
 DR SMART; SM00277; GRAN; 1.
 DR PROSITE; PS00640; THIOL_PROTEASE_ACN; UNKNOWN_1
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1
 KW Protease.
 FT NNN TER
 SQ SEQUENCE 445 AA; 44414 MW; E80437E45C1A1D9 CPO64;
 Query Match 23.1%; Score 392.5; DP 10; Length 445;
 Best Local Similarity 23.1%; Pct Id 75; Mismatches 135; Indels 37; Gaps 11;
 Matches 98; Conservative 68;
 QY 3 IVLAIAIHALSAV--YAPPESTVTFEYFYAFNFSYATFEDEAAAPFELESVYVYVSN 60
 DB 12 VLLASSELGWTATAPENFEVPMERWLVENHAYNGDGEHFFPELPMNLKPVQSH 71
 QY 61 CGAIN-- HLCGATSTSEPIPELMAFAFPHLPTFDLMATNACDINGKAPAE 112
 DB 72 NSVPNQSVFLGTPFADLTTPFAPIYLPSS---PMPTPDSVSPSYLHNVDKLPDEV 127
 QY 113 ELRQMTVTPIRMQGGGGSSWAFSSVAATSAVLAVNGNSLAPDELVQASCH--GTH 170
 DB 128 ENRAFAVTVTFGAT--TAWAA--AA--DAV--SH--HPLDELVQCELELVDESHHHSS 197
 QY 171 QETTRTFEYTHHNVY--ESYFYVAFPS--T--SHACAFDSEHNS--LYPPKPKKE 211
 DB 188 GRLMAYAFQFIISNGDTEDEYVIAIDNLCNTOKNTFVVIIGYFQV--PENFSLK 244
 QY 227 EALACTSIAIVAGISIELLAFAH--YGGFTIIGRNGYV--NHAVNYVYVNA--VGVW 244
 DB 247 KALANQPSVAIEAGSPFQYKSGVETGTGUALD-----HGVAVAVYGTSEGGYV 299
 QY 245 IVNSMOTNMGNGYGFPAAMI-----DLMMIEYP 315
 DB 300 IIRNSWSGNSGSEYVLENIHSSKQVAVMASIP 417
 RESULT 6
 Q95VA7 PRELIMINARY; PRT; 326 AA.
 AC Q95VA7
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cathepsin L.
 GN CAT-LIG.

OS Fasciola gigantica.
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Euhaptorhiza; Platyhelminthes; Fasciolidae; Fasciola.
 GN Fasciola gigantica; Fasciolidae; Fasciola.
 NCBI_TaxID=46895;
 [1]
 SEQUENCE FROM N.A.
 RA Subbot F., Meenen K., Glans R., Glans C.V., Rojce G., Hofmann A.;
 RT "Molecular cloning of Cathepsin L encoding genes from Fasciola
 RT gigantica.",
 DR EMBL; AF13229; AAL23917.1;
 DR InterPro; IPR000669; Peptidase_C1
 DR InterPro; IPR000169; Suppt_actin
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR ProDom; PD000158; Peptidase_C1; 1.
 DR PROSITE; PS00640; THIOL_PROTEASE_ACN; UNKNOWN_1
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1
 KW Protease.
 FT NNN TER
 SQ SEQUENCE 326 AA; 37457 MW; 7C3F42E748E64EE1 CPO64;
 Query Match 23.1%; Score 389.5; DP 5; Length 326;
 Best Local Similarity 31.9%; Pct Id 25; Mismatches 109; Conservative 56;
 Matches 109; Conservative 56; Mismatches 109; Indels 42; Gaps 15;
 QY 5 LATASLLASAVYAKFSSSTFEYFYAFNFSYATFEDEAAAPFELESVYVYVSN 61
 DB 3 LFLITVL LAGAPA SHDELWHEWPEYFNFGACNEH PPTVWPEYFNFGACNEH 57
 QY 62 -- GAINHSLSTLSDSEPIPEL--MAFAFPHLPTFDLMATNACDINGKAPAE 110
 DB 59 HILGLVTVTFGAT--TAWAA--AA--DAV--SH--HPLDELVQCELELVDESHHHSS 110
 QY 111 EIDLQMTVTPIRMQGGGGSSWAFSSVAATSAVLAVNGNSLAPDELVQASCH--GTH 166
 DB 111 SIDMQGVYVTEVNAQGGSSWAFSSVAATSAVLAVNGNSLAPDELVQCELELVDESHHHSS 169
 QY 167 HTHHTTTHGFTVTPVAVV--SYFYVAFPS--T--SHACAFDSEHNS--LYPPKPKKE 211
 DB 170 HPSGQMMENHAYV--YGGFTIIGRNGYV--NHAVNYVYVNA--VGVW 227
 QY 224 EIFEALACTSIAVAGISIELLAFAH--YGGFTIIGRNGYV--NHAVNYVYVNA--VGVW 283
 DB 229 ELK2MVGFQFPAVATAGP--FWTHESINMGVETTRVTHAVAVYGTSEGGYV 284
 QY 284 WIVRNDWTHMGNGYGFPAAMIDLM-----DLMMIEYP 315
 DB 285 WISKNSGNSGSEYVLENIHSSKQVAVMASIP 326
 RESULT 7
 Q24944 PRELIMINARY; PRT; 326 AA.
 AC Q24944; P91728;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Cathepsin L-like protease (Fasciola gigantica; Fasciola L. like)
 GN ECL2.
 OS Fasciola hepatica (Liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Euhaptorhiza; Platyhelminthes; Fasciolidae; Fasciola.
 GN Fasciola hepatica; Fasciolidae; Fasciola.
 NCBI_TaxID=6192;
 [1]
 SEQUENCE FROM N.A.
 RA Heussler V.T., Dobbelaere D.A.E.;
 RT "Cloning of a protease gene family of Fasciola hepatica by the
 RT polymerase chain reaction.",
 AL Mol. Biochem. Parasitol. 64:11-23(1994).
 GN CAT-LIG.
 KW Protease.
 FT NNN TER
 SQ SEQUENCE FROM N.A.
 MEDLINE-97418901; PubMed-9274877;

DE Thiol protease precursor.
 OC Phaedon cochleariae (Mustard beetle).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Beoptera; Polypterygota; Coleoptera; Polyptaga.
 OC Cucujiformia; Phytoptera; Chrysomelidae; Chrysomelidae;
 OC Chrysomelinae; Eneaden.
 OC NCBI_taxid=40247;
 RN [1]
 RN SEQUENCE FROM N.A.
 PC TISSUE=GUT;
 RA Girard C., Jouanin L.;
 BL Submitted (AUG 1998) to the EMBL/GenBank/CCDB databases.
 DE EMBL; Y17903; CAA76927.1; ..
 DR HSP; O60911; LFH0.
 DR InterPro; IPR000669; Peptidase_C1.
 DR Pfam; PF00112; Signal site.
 DR PRINTS; PR00705; PAPAIN_1.
 DR PROSITE; PS00158; Peptidase_C1; 1.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNWN_1.
 DR PROSITE; PS00634; THIOL_PROTEASE_HIS; UNKNWN_1.
 KW Protease; Signal.
 FT SIGNAL 1 16 POTENTIAL
 FT CHAIN 110 324 THIOL PROTEASE
 SQ SEQUENCE 324 AA; 35458 MW; 5E0F191D2C84067F CRC64;
 Query Match 22.6%; Score 381; DR 5; Length 324;
 Best local similarity 21.6%; Prod. No. 2.2e 24;
 Matches 102; Conservative 119; Mismatches 119; Indels 46; Gaps 15.
 QY 1 MFIYVATASLALGAVYAPGSSHTPEETVYAFNKSVAATPEDEAAENP 52
 DE 1 MLIHIALAALG---VWNAAG---LWMAKPKTHATYKSLR-BEKLPEHIF-ITLPQIAE 56
 QY 53 EYAYVSGMSS ALPHISLSLSEFPENPELM-AFA---PHLPTQFMAETNAAT 100
 DE 57 HNVK---ENFSTHVALNFSQITPEFPEP-MEMNAAPNENRVA-HIV----- 100
 QY 123 SINWAFATETIR-PEYVYTRFEM-SSSSGFWAESGVATISAYLAVPNSGLLAELVYS 102
 DE 104 ---GAAPENILWPKKVVLPVFN-R-FG-SWASTAAKPS-CAIFSGSKVPLSPQLVD 164
 QY 163 TAC QETHTGILHRIHILGHPSTVYSYVYVARE-SEPPHMAE---FISHVETI 217
 DE 165 GSTVCHNCHGAVGAFGPEYVYVNGDIPSSAWPYSYFERYVAVKVPQFWELT-VYV 224
 QY 219 VPPVNVKTPDEALACTHCAIAVILGIVOLDAPPHYVGGTIIQPDNGYQPN VYAVNVGVYS 276
 DE 225 TACTGCKEAYVGTIGFICATVPS FMYKSYSSSIFSSSELGILHSHVETVJG 278
 QY 277 NAQVYVYVENSWMINWNGUNY 299
 DE 279 IENGKQVWIKNTGAWGESSY 301
 RESULT 10
 QYQZH7
 IC QYQZH7 PRELIMINARY; EX1; 348 AA.
 AC QYQZH7
 DI 01-MAY-1999 (Trembl) 10; (created)
 DT 01-MAY-1999 (Trembl) 10; Last sequence update)
 DT 01-NOV-2002 (Trembl) 25; Last annotation update)
 DE Putative cysteine proteinase.
 GN AT232742
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosales II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_taxid=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 PC STRAIN=CV. COLUMBIA;

RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Pounsley S.D., Shea T.F., Benito M.L., Town C.D.,
 PA Fujii C.V., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 EA Bell C.E., Ketchum K.A., Lee J.Z., Zaitlin S.M., Kuo H., Moffat K.S.,
 PA Cronin L.A., Shen M., VanAken S.E., Enayati L., Tallon L.D., Gill J.R.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana";
 RL Nature 402:761-768(1999).
 RN [2]
 RN SEQUENCE FROM N.A.
 PC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 BL Submitted (MAR 2000) to the EMBL/GenBank/CCDB databases.
 DE EMBL; AF064333; AAL36383.1; ..
 DR HSP; P07711; ICJL.
 DR InterPro; IPR000668; Peptidase_C1.
 DR InterPro; IPR000169; SHprol acsite.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR PRINTS; PR00705; PAPAIN_1.
 DE Pfam; PF00158; Peptidase_C1; 1.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00634; THIOL_PROTEASE_HIS; UNKNWN_1.
 KW Hydrolase; Thiol protease.
 SQ SEQUENCE 348 AA; 38738 MW; EB86ABECB53E76 CRC64;
 Query Match 32.5%; Score 390.5; DP 10; Length 348;
 Best local similarity 32.5%; Prod. No. 2.2e 24;
 Matches 116; Conservative 50; Mismatches 132; Indels 57; Gaps 18;
 QY 1 MKVILATASLALS-AVAPPSSIKTFEEVYKAPKSVATPEDEAAENP 53
 DE 9 LTIFLSYPTSLATSPGSLFEAPALKEHEQWAPENRVS---PETEFENPEHIFKNLEF 65
 QY 54 VYVYVSGGA-----INHLSDLSLSEK---NDPLMSAEAFELHTQFDINARTNA----- 101
 DE 66 VQNPNNNTYVYVDINERFSLTLEEFKPAHTLSLVVPEALTFST---ISSGFNIVPKRY 122
 QY 100 ---CSINQNAFAFTELQMPYVTFIPW-SS-SWAFEGYVAVTERAVLAVFN-LLGLAS 159
 DE 123 INVVDGSS---MELPS-EGAVTPVYV-LP-LG-SWASAAVAVGHTITKSPV-LSLQ 179
 QY 160 LVLGASDH---GSHSTPTPGIEY-LHNSGVVSESYFYVARESGCFENNA-----QPF 211
 DE 180 LLGLTFVNSG-EDPDMSPAFVILNLTITFQVYVYFSGSTPS-PTNS---PAAT 239
 QY 212 SHGQVYFPPVNRKRLALATHEALAVLISGLD AHHHDKILLQKST QFNH 268
 DE 240 GGY-ETVMS---NEEALLAVGQVGVSLSTJAAPPHSGAV NEEGTELLH 291
 QY 263 AVNVGVYS NAQGVYVYVENSWMINWNGUNYGYFAAT-----LWVDEYF 315
 DE 292 AVTVGMSSEGTHTVWVNSWETWNGSNIRPHFVCEVAFSGMGLALATFP 346
 RESULT 11
 Q8T0X0

Search completed: March 12, 2002, 11:23:34
Job time : 74.1706 secs

GenCore version 5.1.4 p5.470
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GM protein - protein search, using sw model

Run on: March 11, 2003, 15:11:59, Search time 80.8027 seconds
(without alignments)
527,709 William cell updates/sec

Title: US-09-877-160-2

Perfect score: 1689
Sequence: 1 METVLASIALCAVAYAP

Scoring tables: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 11250620 residues

Total number of hits satisfying chosen parameters 908470

Minimum DB seq length: 0

Maximum March 100%

Post processing: Minimum Match: 0%

Listing first 45 summaries

Result No.	Score	Query Match	Length	EB	ID	Description
1	1689	100.0	320	20	AAV2580	D. pteronyssinus
2	1689	100.0	320	20	AAV2580	D. pteronyssinus
3	1689	100.0	320	20	AAV2580	D. pteronyssinus
4	1689	99.5	320	20	AAV2580	D. pteronyssinus
5	1679	99.4	320	20	AAV2580	D. pteronyssinus
6	1677	99.3	320	15	AAV2580	Protein allergen
7	1650.5	97.7	316	20	AAV2580	D. pteronyssinus
8	1612	95.4	302	22	AAV2580	D. pteronyssinus
9	1612	95.4	302	22	AAV2580	D. pteronyssinus
10	1608	95.2	302	22	AAV2580	D. pteronyssinus

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

11	1608	95.2	302	22	AAV2580	Recombinant dust m
12	1608	95.2	302	22	AAV2580	D. pteronyssinus m
13	1608	95.2	302	22	AAV2580	D. pteronyssinus m
14	1592.5	93.7	339	20	AAV2580	D. pteronyssinus m
15	1453.5	86.1	321	22	AAV2580	E. maynei Group 1
16	1433.5	84.9	321	22	AAV2580	Recombinant Derf1
17	1433.5	84.9	321	16	AAV2580	Recombinant Derf1
18	1433.5	84.9	330	16	AAV2580	Recombinant mite a
19	1425.5	84.4	321	13	AAV2580	Der f 1 allergen.
20	1425.5	84.4	321	14	AAV2580	Recombinant mite f
21	1425.5	84.4	321	15	AAV2580	Protein allergen o
22	1425.5	84.4	321	15	AAV2580	Der f 1. Dermatop
23	1425.5	84.4	321	19	AAV2580	Dermatophagoides D
24	1425.5	84.4	321	22	AAV2580	Dermatophagoides S
25	1425.5	84.4	321	22	AAV2580	D. farinae Group 1
26	1425.5	84.4	321	22	AAV2580	House dust mite al
27	1396.5	82.7	319	20	AAV2580	D. farinae allergen
28	1396.5	82.7	322	22	AAV2580	E. maynei Group 1
29	1368.5	81.0	303	16	AAV2580	Recombinant Derf1
30	1368.5	81.0	303	16	AAV2580	Recombinant Derf1
31	1367.5	81.0	302	22	AAV2580	D. farinae Der f 1
32	1367.5	81.0	304	21	AAV2580	Tick allergen ber
33	1360.5	80.6	303	22	AAV2580	D. farinae Group 1
34	1360.5	80.6	303	22	AAV2580	D. farinae Der f 1
35	1357.5	80.4	303	22	AAV2580	D. farinae Der f 1
36	1354.5	80.2	303	22	AAV2580	D. farinae Der f 1
37	1313	77.7	245	12	AAV2580	Der p 1 allergen.
38	1313	77.7	245	14	AAV2580	Dermatophagoides p
39	1313	77.7	245	15	AAV2580	Protein allergen o
40	1313	77.7	245	15	AAV2580	Der p 1. Dermatop
41	1313	77.7	245	15	AAV2580	Der p 1 allergen.
42	1313	77.7	245	15	AAV2580	Dermatophagoides D
43	1313	77.7	245	15	AAV2580	Dermatophagoides S
44	1313	77.7	245	22	AAV2580	House dust mite al
45	1271.5	73.3	181	16	AAV2580	Recombinant Derf1

ALIGNMENTS

RESULT 1

AAV2580

10 AAV2580 standard; protein; 320 AA.

XX AAV2580;

XX AAV2580;

XX 30-SEP-1999 (first entry)

XX D. pteronyssinus allergen Der p 1 protein fragment.

XX Major histocompatibility complex, class II, desensitizing; human;
allergen; glass, tree, wool, pollen, food, mold, food, insect, sting;
chironomids, spider, mite, housefly, fruit fly, sheep blow fly, honeybee;
screw worm fly; grain weevil; silkworm; bee mite; larvae; woolworm; cat;
cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

XX Dermatophagoides pteronyssinus.

XX WO934826-A1.

XX 15-JUL-1999.

XX 11-JAN-1999; 40W-0800000.

XX 21-SEP-1998, 90GB 0000474.

XX 09-JAN-1998, 90GB 0000445.

XX (PM70-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Ray AP, Larche M;

XX WI, 1999-455-05/38.

Example 1: P17 21, 98pp, English.

AA849020 is a preproenzyme Derp1. The amino acid sequence preceding the mature protein sequence contains cleavage sites for the pro- and proenzyme forms, with residues 1-97 corresponding to a partial signal peptide sequence. The mature protein can be used to detect sensitivity in an individual to house dust mite and to reduce the sensitivity of the individual.

Sequence 320 AA;

Query Match 99.38; Score 1677; DB 15; Length 320;
 Best Local Similarity 99.38; Pred. No. 3 aa-164;
 Matches 317; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 1 MKIVLALSLALSAVAPRPSSTPTFEYYPAPNPKSVATFEDSEAPKPLESVYVQSN 60
 1 MKIVLALSLALSAVAPRPSSTPTFEYYPAPNPKSVATFEDSEAPKPLESVYVQSN 60
 61 GGAINHLSLSLEPPRFIMSAFAEHLTPTFELNAFTNACSTPNAPAEIDLPMPETV 120
 61 GGAINHLSLSLEPPRFIMSAFAEHLTPTFELNAFTNACSTPNAPAEIDLPMPETV 120
 121 TPIRMGGGSCWAFSGVAATESAYLAVENSLALAEGLAVICASLGS 180
 121 TPIRMGGGSCWAFSGVAATESAYLAVENSLALAEGLAVICASLGS 180
 121 TPIRMGGGSCWAFSGVAATESAYLAVENSLALAEGLAVICASLGS 180
 181 IGHNGVQESYYPVAPRPSSTPTFEYYPAPNPKSVATFEDSEAPKPLESVYVQSN 240
 181 IGHNGVQESYYPVAPRPSSTPTFEYYPAPNPKSVATFEDSEAPKPLESVYVQSN 240
 241 GIKLDAFRHYEGRIITIGPENGYFNTHAVNIVTSMAQSGVGVWIVNSWETNWSJNG 300
 241 GIKLDAFRHYEGRIITIGPENGYFNTHAVNIVTSMAQSGVGVWIVNSWETNWSJNG 300
 301 YFAANIDLMMEIEYYPVVIL 320
 301 YFAANIDLMMEIEYYPVVIL 320

RESULT 7

AA849020

AA849020 standard; Protein; 315 AA.

AA849020;

AA849020;

05 AUG 1999 (first entry)

05 AUG 1999 (first entry)

D. pteronyssinus Derp1 allergen deletion mutant protein.

Allergen; Derp1; house dust mite; anti-allergic; immunosuppressive; mast cell degranulation; interleukin-4 synthesis; allergen-specific IgE; interleukin-4 secretion; allergy; treatment; vaccine; mutant.
 Thi type immune response; Derp1 specific IgG

Dermatophagoides pteronyssinus.

Synthetic.

W09925823-A2.

27 MAY 1999.

16 NOV 1998; 98W0-EP0721

19 NOV 1997; 97GB-0024531.

(SMK) SMITHKLINE BEECHAM BIOLOGICALS.

Bollen A, Bruck C, Jacobs P, Mascuer M;

WPI; 1999-347471/29.

N FCBP; AA849020.

Recombinant mutant Derp1 allergen with reduced enzymatic activity
 Claim 12, Page 41-42, 46pp; English.
 This invention describes novel recombinant mutant allergens derived from the dermatophagoides pteronyssinus (dust mite) Derp1 allergen which have reduced enzymatic activity compared to the wild type allergen and are anti allergic and immunosuppressive. The allergens induce mast cell degranulation to stimulate interleukin 4 synthesis and secretion, even in the absence of allergen-specific IgE. The mutant allergens are useful in manufacture of medicaments for the treatment of allergy. Vaccines comprising the mutant allergens are useful for treatment or prevention of allergic responses, particularly to house dust mite. The mutant allergens increase the Th1-type aspect of immune responses in comparison to those stimulated by the wild-type allergen, leading to the suppression of allergic potential of the vaccinated host. They also have reduced allergenicity and are hence more suitable for systemic administration at high doses. The mutant allergens also induce Derp1 specific IgG which compete with IgE for the binding of native Derp1.

Sequence 315 AA;

Query Match 97.74; Score 1650.5; DB 20; Length 315;
 Best Local Similarity 98.48; Pred. No. 190 161;
 Matches 315; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
 1 MKIVLALSLALSAVAPRPSSTPTFEYYPAPNPKSVATFEDSEAPKPLESVYVQSN 60
 1 MKIVLALSLALSAVAPRPSSTPTFEYYPAPNPKSVATFEDSEAPKPLESVYVQSN 60
 61 GGAINHLSLSLEPPRFIMSAFAEHLTPTFELNAFTNACSTPNAPAEIDLPMPETV 120
 61 GGAINHLSLSLEPPRFIMSAFAEHLTPTFELNAFTNACSTPNAPAEIDLPMPETV 115
 121 TPIRMGGGSCWAFSGVAATESAYLAVENSLALAEGLAVICASLGS 180
 116 TPIRMGGGSCWAFSGVAATESAYLAVENSLALAEGLAVICASLGS 175
 181 IGHNGVQESYYPVAPRPSSTPTFEYYPAPNPKSVATFEDSEAPKPLESVYVQSN 240
 176 IGHNGVQESYYPVAPRPSSTPTFEYYPAPNPKSVATFEDSEAPKPLESVYVQSN 235
 241 GIKLDAFRHYEGRIITIGPENGYFNTHAVNIVTSMAQSGVGVWIVNSWETNWSJNG 300
 236 GIKLDAFRHYEGRIITIGPENGYFNTHAVNIVTSMAQSGVGVWIVNSWETNWSJNG 295
 301 YFAANIDLMMEIEYYPVVIL 320
 296 YFAANIDLMMEIEYYPVVIL 315

RESULT 8

AA849020

AA849020 standard; Protein; 302 AA.

AA849020;

AA849020;

21 AUG 2001 (first entry)

D. pteronyssinus Derp1 protein fDerp1-302.

Mite group 1 protein, methylophilic yeast, Escherichia coli, allergy; recombinant mite group 1 protein, allergic response, anti-allergic; infectious disease, allergic disease.

Dermatophagoides pteronyssinus.

W099127078 A2.

26 APR 2001.

12 OCT 1999; 1999W-0119-04.

Search completed. March 12, 2003. 16:33:11
Job time : 54.4415 secs

GenCore version 5.1.4 ps 4578
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QM protein - protein search, using sw model

Run on: March 12, 2003, 09:22:06 : Search time 32 4716 seconds
(without alignments)
926 417 million cell updates/sec

Title: US-09-877-160-3
Perfect score: 773
Sequence: 1 MWAFHTTSLHVAWAPGV.....VMSEGVLAIAIAHVAIPV 146

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Sorted: 671580 hits, 206347115 residues 671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match 94
Maximum Match 100

Listing first 45 summaries

Database: 1: SPREMBL 21:

- 1: sp_archaea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mhc:
- 8: sp_organelle:
- 9: sp_phage:
- 10: sp_plant:
- 11: sp_rent:
- 12: sp_virus:
- 13: sp_vertebrate:
- 14: sp_unclassified:
- 15: sp_virus:
- 16: sp_bacteriophage:
- 17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649.5	84.0	170	5	Q9BIX2 dermatophag
2	626	80.9	170	5	Q9BIX2 dermatophag
3	106.5	39.7	143	5	Q965E2 psoroptes
4	273	35.3	125	5	Q9BIX4 glycyphagus
5	249	32.2	128	5	Q9BIX7 glycyphagus
6	115.5	14.9	186	5	Q9BIX1 caenorhadi
7	103	13.3	165	5	Q9BIX3 drosophila
8	83	10.7	160	5	Q9BIX7 drosophila
9	80.5	10.4	1245	12	Q9BIX7 drosophila
10	79.5	10.3	414	13	Q9BIX7 drosophila
11	79.5	10.3	2643	5	Q9BIX4 caenorhadi
12	73	10.2	167	5	Q9BIX4 drosophila
13	73	10.2	171	5	Q9BIX3 drosophila
14	78.5	10.2	153	13	Q9BIX4 caenorhadi
15	78.5	10.2	292	13	Q9BIX4 caenorhadi
16	78.5	10.2	574	13	Q9BIX4 caenorhadi

17	78	10.1	249	15	Q55394
18	78	10.1	381	2	Q9BIX2
19	77	10.0	154	5	Q9BIX2
20	76.5	9.9	477	2	Q9BIX2
21	76.5	9.9	565	2	Q9BIX2
22	76.5	9.9	936	16	Q9BIX2
23	76.5	9.9	381	2	Q9BIX2
24	76.5	9.9	410	12	Q9BIX2
25	75.5	9.8	896	16	Q9BIX2
26	75.5	9.8	6875	6	Q9BIX2
27	75	9.7	1026	5	Q9BIX2
28	74.5	9.6	411	5	Q9BIX2
29	74	9.6	381	2	Q9BIX2
30	74	9.6	381	2	Q9BIX2
31	74	9.6	381	2	Q9BIX2
32	74	9.6	381	2	Q9BIX2
33	74	9.6	381	2	Q9BIX2
34	74	9.6	381	2	Q9BIX2
35	74	9.6	381	2	Q9BIX2
36	74	9.6	381	2	Q9BIX2
37	74	9.6	381	2	Q9BIX2
38	74	9.6	381	2	Q9BIX2
39	73.5	9.5	2103	13	Q9BIX2
40	73	9.4	381	2	Q9BIX2
41	73	9.4	381	2	Q9BIX2
42	73	9.4	407	17	Q9BIX2
43	73	9.4	407	17	Q9BIX2
44	73	9.4	664	4	Q9BIX2
45	73	9.4	1188	5	Q9BIX2

ALIGNMENTS

RESULT 1

Q9BIX2 PRELIMINARY: PRT: 170 AA.

AC Q9BIX2; 01-JUN-2001 (TREMELrel. 17, Created)

DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)

DE Allergen Def f II (fragment)

OS Dermatophagoides farinae (House-dust mite)

EC Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari

CC Acariformes, Sarcoptiformes, Astigmata, Analgoidea, Pyroglyphidae

OC Dermatophagoides

OX NCBI_TaxID=6954

RN [1]_SEQUENCE FROM N.A.

RA HAO M., Xu J., Zhong N.

RE PubMed:11111111; FFP:11111111; FFP:11111111; FFP:11111111

DR EMBL: AF346905; AAK30133.1; -

DR HSSP: Q00855; 1AHK

DR InterPro: IPR003172; E1_DerP2_DerP2

DR Pfam: PF02221; E1_DerP2_DerP2

FT NON_TER 1

SQ SEQUENCE 170 AA: 18781 MW: 602556734C9D443A CRC64;

Query Match 84.0%, Score 649.5, DB 5, Length 170,

Best Local Similarity 72.9%, Pred. No. 4.1e 61,

Matches 124, Conservative 11, Mismatches 6, Indels 23, Gaps 14

Q9BIX2 LLSLLVAVAVADQVDVDC AHHHKKVDP 36

DB LLSLLVAVAVADQVDVDC AHHHKKVDP 60

Q9BIX2 Q9BIX2 LLSLLVAVAVADQVDVDC AHHHKKVDP 36

DB Q9BIX2 Q9BIX2 LLSLLVAVAVADQVDVDC AHHHKKVDP 60

Q9BIX2 Q9BIX2 LLSLLVAVAVADQVDVDC AHHHKKVDP 120

DB Q9BIX2 Q9BIX2 LLSLLVAVAVADQVDVDC AHHHKKVDP 146

Q9BIX2 Q9BIX2 LLSLLVAVAVADQVDVDC AHHHKKVDP 170

DB Q9BIX2 Q9BIX2 LLSLLVAVAVADQVDVDC AHHHKKVDP 170

Matches 54; Conservative 43; Mismatches 46; Indels 3; Gaps

CY 1 MWVYLKSLVAARFQVEVFCAHHEIPPVVPFHCHCEPTTTPRPPPEFAVFFA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MWHLVLAILTLAVVSAGAPVFPFGDFGFEVEREVEESST EVVDGGPFIATLADMT 59

CY 61 KNTYTATHIEIFASTIGLELVVGSIENIAHYMKCTIIVPGECIDITHTWTVPIAFGEN 100
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 60 KDCACALKEIQVALDMGVNTEVVGTHTTHVHPFTPTVHQEVVTAKETPAEFIFA 119
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

CY 121 VVVVVVMGDGCVIACAIAAHATPAD 146
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 120 KY AVTGDSHGSC-IVINGEQD 143
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
Q9NF04 PRELIMINARY; PRT; 125 AA.
ID CONFO4
AC Q9NF04:
DT 01-OCT-2000 (TrEMBLrel 15, Created)
DI 01-OCT-2000 (TrEMBLrel 18, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel 19, Last annotation update)
OS Gly d 2.02 isoform (fragment).
OC Glycophagus domesticus.
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
AA Acanthiformes; Sarcoptiformes; Asigmatia; Glycyphagidae; Glycyphaginae;
OX NCBI_TaxId=105145;
RN [1]
RP SEQUENCE FROM N.A.
FX MEDLINE C11380C, PubMed=110405;
PA Gavellin G., Johansson B., Lundin A., Smith A.M., Chapman M.D.,
Pettersen R.C., Pettersen J., van Halbeek H.;
BT crosses reactivity studies of a new group 2 allergen from the dust mite
glycophagus domesticus. Gly d 2.02 isoform: 2 allergens from
dermatophagoides pterocarpinus, Lepidoglyphus destructor, and
Tyrophagus putrescentiae with recombinant allergens.";
RL J. Allergy Clin. Immunol. 107:511-518(2001).
CP FMRU; AJ273216; CAB76456 1; -;
DR HSPB; Q00855; 1AHK.
DR InterPro: IPRO00172; El_DerP2_DerF2.
DR Pfam: PF02221; El_DerP2_DerF2 1.
FT NON TER 1
SQ SEQUENCE 125 AA; 13366 MW; 61607DDCFRDADF0 CP064;

Query Match: 35.0%, Score 273, DB 5, Length 125,
Best Local Similarity: 45.6%, Prof No. 5, 9e 21;
Matches 52; Conservative 31; Mismatches 16; Indels 3; Gaps

CY 10 PTVAHIEPFVDPVGHSEPTINPHSEELPAVFANMNTTTFATETASTETEVSV 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6 KCGDGVEVELDTCSS DPQVIHPSELTETEAFFASSTTKATTATPATACTICV 64

CY 92 ESIRGNACHMYCKPLAWGCQVGYIKWTNVRYIAHSNNVYVPMGFQDVAC 136
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 65 PSLETGGSEFWTFEPSEPTISPTTSFTTTTVAILEPYV AYETAELMDQLULAC 117

RESULT 5
Q9USP7 PRELIMINARY; PRT; 128 AA.
ID Q9USP7
AC Q9USP7:
DT 01-MAY-2000 (TrEMBLrel 13, Created)
DE 01-MAY-2000 (TrEMBLrel 13, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel 19, Last annotation update)
OS Gly d 2 (Fragment).
OC Glycophagus domesticus.
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
AA Acanthiformes; Sarcoptiformes; Asigmatia; Glycyphagidae; Glycyphaginae;
OX NCBI_TaxId=105145;
RN [1]
RP SEQUENCE FROM N.A.

Query Match: 37.7%, Score 306.5, DB 5, Length 143,
Best Local Similarity: 37.0%, Prof No. 9, 3e 25;
Matches 112; Conservative 10; Mismatches 4; Indels 0; Gaps

CY 16 TQQVPTTAHMEIPPWVFSIHSEPTTHPSFEGLAVFEAMNTTPTATETASTET 77
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 QVADVPTANTHELPAVMTCTGCTGP-IHP-VPTTEALEPDALTPTATETASTET 60

CY 18 LREKQNTQNNAHWMPTRVDFDLTIIFTTWNPYPIAFSENVVTVTVWITVLAIA 130
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 LRIPVLSHTWAHPMVSDVFDGCVAFITWWNPYPIAFSENVVTVTVVLDVQVLA 120

CY 139 IATAHXKD 146
|||||||
DB 121 IATAHXKD 129

RESULT 3
Q965E2 PRELIMINARY; PRT; 143 AA.
ID Q965E2
AC Q965E2:
DI 01-DEC-2001 (TrEMBLrel 19, created)
DT 01-DEC-2001 (TrEMBLrel 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel 20, Last annotation update);
ALLergen A precursor.
OG ALLA.
OS Psoroptes ovis (sheep scab mite).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
AA Acanthiformes; Sarcoptiformes; Asigmatia; Glycyphagidae; Glycyphaginae;
OX NCBI_TaxId=83012;
RN [1]
RP SEQUENCE FROM N.A.
RA Temeyer K.B., Solleau L.G.;
RT "Sequence of a cDNA encoding a precursor of a major allergen of
Psoroptes ovis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RW EMBO, ARS-1993, ABX1827.1,
DR InterPro: IPP00172; El_DerP2_DerF2
DR Pfam: PF02221; El_DerP2_DerF2 1.
KW Signal.
FT SIGNAL 1 17 POTENTIAL
FT CHAIN 16 143 ALLERGEN A
SQ SEQUENCE 143 AA; 16217 MW; AP0143GSGAPASAD CP064;

Query Match: 37.7%, Score 306.5, DB 5, Length 143,
Best Local Similarity: 37.0%, Prof No. 9, 3e 25;
Matches 112; Conservative 10; Mismatches 4; Indels 0; Gaps


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DR InterPro: IP0003170; El DerP2 DerP2.
DR Pfam: PF00221; El_DerP2_DerP2_1.
SC SEQUENCE 155 AA, 19562 MW, 78AA:90CD125CE5T CRG64,
Query Match 13.3%; Score 103; DB 5; Length 165;
Best Local Similarity 24.7%; Pred. No. 0.0044;
Matches 38; Conservative 31; Mismatches 55; Indels 10; Gaps 9;
QV: 5 LCLLLVAVAPQOVYKDCARHEIKK --LVVGHGHCENCCHHKCFQCAENTAVNC 62
DB 11 LVTFTMTGTA--GTRTFSCAGNCPY:WVQIDCC DALPTLTWGTAKIDIFVATP 68
QV 52 NRTAFATFVASHSFHVYV-----GIDFNACHVWVPLVGLQVDFYV-----T 109
DB 69 NT-MKLSAEVHLISLVITPYDLEAS:SNVSNLHJAVCFDAGE--SVTYQLLPVT 125
QV 100 WNVFKIAPKSNVYVWVWVWVWGNG---VLACATA 134
DB 100 TCTCEVTEIE...VELLSGDSNENSVGCELA 154
RESULT 9
QVNT7
ID QVNT7 PRELIMINARY; PPT: 119 AA.
AC QVNT7;
DT 01-MAY-2000 (TRENBLrel 13, Created);
DT 01-MAY-2000 (TRENBLrel 13, Last sequence update);
DT 01-MAY-2000 (TRENBLrel 13, Last annotation update);
DE CG153 protein (R336503p);
GN CG153
OS Drosophila melanogaster (fruit fly)
OC Eukaryota, Metazoa, Arthropoda, Insecta,
OC Prochordata, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
OC Ephyridia, Ephyridiidae, Drosophilidae,
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikor S.E., Holt B.A., Evans C.A., Gecayze J.D.,
RA Ananidis P.G., Scherer S.E., Li P.W., Hopkins P.A., Galle P.F.,
RA George R.A., Lewis S.E., Richards R., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
RA Paterson B.C., Poyet Y.H.C., Blazer P.G., Champ M., Pfeiffer B.D.,
RA Wan Y.H., Doyle C., Baxter E.G., Holt G., Nelson C.B., Miklos G.L.G.,
RA April J.P., Agbayani A., An H.J., Andrews Pankoch C., Baldwin P.,
RA Balow P.M., Bacu A., Baxendale J., Bayraktarcu L., Beasley E.M.,
RA Beeson V.Y., Pence F.V., Rottin B.P., Rhoadri P., Solchaker S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Purris K.C., Busan D.A., Pukler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson V., Dupl E., Doves M., Dugan Pocha S., Dunkov B.C., Dunn F.,
RA Durbin J., Ewingolista C.C., Fierro C., Fierro S., Fleischmann W.,
RA Fowler C., Garmel A.E., Garg N.S., Gaibart W.M., Glasser K.,
RA Glaser A., Gong F., Gortel J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiland T.J., Hernandez J.P., Hock J.,
RA Hostin K., Houston K.A., Howland T.J., Wei M.-H., Ibegwan K.A.,
RA Jalali M., Kalush F., Karp G.H., Ye Z., Kennison J.A., Korchun K.A.,
RA Kimmel R.P., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li Z., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Malshina N.V., Mobarty C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy E., Murphy L., Murry D.M., Nelson D.L.,
RA Nelson C.P., Nelson K.A., Nivon K., Nusser D.P., Pachel J.M.,
RA Pallazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Peiner K., Penington K., Saunders P.D.C., Schoeler P., Shen H.,
RA Shue B.C., Sideri-Ammas I., Simpson M., Skupski M.P., Smith T.,
RA Spier F., Spradling A.C., Stappleton M., Strong P., Sun F.,
RA Sviridov P., Teeter C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang C.W., Wassman T.A., Weinreb J.V., Weissman J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Yaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,

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Query Match 10.7%; Score 93; DB 5; Length 159;
Best Local Similarity 23.5%; Pred. No. 0.157;
Matches 33; Conservative 25; Mismatches 45; Indels 30; Gaps 8;
QV 5 LCLSLVAAVA PCTVWVPCNHPV PVVVGTHSFFTHHFFPQIPA 54
DB 5 LSLVFTFARLIPTSTONS2FFVFFALAAVUSINHTFSTTFFENTAFICM 61
QV 57 VFENQNTWAKIEIPASIGCLEVNVQIDP-----NCHY-----MPCLVVQCC 103
DB 61 FTFPFFEL FLSLQGLIICAVIETETSTASATHTVSEAGAFPTTTPVAV 117
QV 103 YDHYVWTFKIAPISENVVTVV MNTGVLAQAIATWATP 145
DB 119 YTVVDFEFTVWP TVSEFHWNGVPHSCAA-FCITAVIV 158
RESULT 9
QVNTX7
ID QVNTX7 PRELIMINARY; PPT: 1245 AA.
AC QVNTX7;
DT 01-MAY-1999 (TRENBLrel 10, Created);
DT 01-MAY-1999 (TRENBLrel 10, Last sequence update);
DT 01-DEC-2001 (TRENBLrel 19, Last annotation update);
DE Structural polyprotein.
OS Sindbis virus
OC Viruses, SSRNA positive strand viruses, no RNA stage, Togaviridae;
OX NCBI_TaxID=11034;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=XJ-160;
RX MEDLINE=20231046; PubMed=10769078;
RA Liang G.D., Li L., Zhou G.L., Fu S.H., Li Q.P., Li F.S., He H.H.,
RA Jin Q., He Y., Chen B.Q., Hou Y.D.;
RA Isolation and complete nucleotide sequence of a Chinese sindbis-like
RA virus.;
RN [2]
RP J. Gen. Virol. 81:1347-1351(2000).
RN [3]
RP SEQUENCE FROM N.A.
STRAIN=XJ-160;
RA Li L., Liang G.D., Zhou G.L., Fu S.H., Jin Q., Hou Y.D.;
RA Submitted (Nov 1998) to the EMBL/GenBank/DBJ databases.
DB EMBL: AF103729; AAC83399.1; -
DB HSSP: P03316; 1KXP
DB InterPro: IPR001936; Alpha_core
DB InterPro: IPR02549; Alpha_E1_glycop.
DB InterPro: IPR00049; Alpha_F2_glycop.
DB InterPro: IPR000533; Alpha_E3_glycop.
DB TrEMBL: PFF01495; P115941.30.
DB InterPro: IPR000930; Togavirin
DB Pfam: PF00344; Alpha_core; 1.

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DR Pfam: PF01589; Alpha E1 glycop; 1.
 DR Pfam: PF00943; Alpha E2 glycop; 1.
 DR Pfam: PF01563; Alpha E3 glycop; 1.
 DR PRINTS: PR00798; TOGAVIRIN
 DR PROSITE: PS00542; PIPISOMAL_S2_1; UNKN-WN_1.
 KW Polyprotein.
 FT CHAIN 1 264 CAPSID PROTEIN
 FT CHAIN 265 328 E3.
 FT CHAIN 329 751 E2.
 FT CHAIN 752 906 E1.
 FT CHAIN 807 1245 E1.
 SO SEQUENCE 1245 AA, 13658 MW, 46.977 kDa, 10.44; 7.44.

Query Match 10.44; Score 80.5; DP 12; Length 1245;
 Best Local Similarity 24.28; Pred. No. 12;
 Matches 32; Conservative 16; Mismatches 44; Indels 39; Gaps 7;

Q1 36 PCHSEIEIILHURKIFLEAVEFAEGRIFIAIEFASIDLEVLVILLI...NA 89
 D1 345 PCHHTEPE-----SPIFELVAPPHPT-TIFLTSAQF----GYGQGATSYNY 291
 Q2 30 CHMAE-----PVENGGALIFVWNP-----FIAPSENWVTVFWKSGG 132
 D1 392 YRVASFQDHTVEGQMTIVIVTSQSPQLCHGVYELLAPPPQS...VTVGVSSSS 449
 Q3 133 VLACAIATHAK 143
 D1 444 LISLIAPAKA 459

RESULT 10

Q1 QJHX6 PRELIMINARY; PRT; 414 AA.
 AC QJHX6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Allantoicase (EC 3.5.3.4).
 GN ALLC OR ALLC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae, Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=CD-1;
 RX METLINE-2125966; PubMed:11440690
 RA Vignetti D., Monetti C., Bernardini G.
 RT "Molecular cloning of mouse allantoicase cDNA (1).";
 RL Biochim. Biophys. Acta 1019:119-121(1991)
 DR EMBL: AF278712; AAF86348.1;
 DR MGD: MGI:2136971; Allc.
 DP InterPro: IPR005164; Allantoicase.
 DR Pfam: PF03561; Allantoicase; 2.
 KW Hydrolase.
 SO SEQUENCE 414 AA, 4.4 kDa, 48.416 kDa, 10.44; 7.44.

Query Match 10.44; Score 79.5; DP 11; Length 414;
 Best Local Similarity 24.28; Pred. No. 4.2;
 Matches 30; Conservative 19; Mismatches 35; Indels 39; Gaps 5;

Q1 33 VLVPGHSGSECTIHRPFCLEAVEFAEGRIFIAIEFASIDLEVLVILLI... 92
 D1 274 LVVPGTEWAVRPAHGVITQIEI...DTYVF
 Q2 33 MAFELVAGGCVY-IFLWNP-----FIAPSENWVTVFWKSGG 140
 D1 313 DGCLITLLEEDMRHWNLPAPHWWSLIPVTVLIPNCHLDELLELD 366
 Q3 141 HAKI 144
 D1 367 HAMI 370

RESULT 11

Q1 QJ1552 PRELIMINARY; PRT; 2643 AA.
 AC QJ1552;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE F47B3.8 protein.
 GN F47B3.8
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoidea; Phlebobranchia; Rhabditidae;
 OC Rhabditidae; Peloderinac; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE:94150718; PubMed:796398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 PA Benfield J., Porton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kerhaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMuray A., Marfisi E., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
 RA Swaidon N., Smith A., Sonnenhammer E., Staden P., Sulston J.,
 PA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinon-Spratt J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 PP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX Du Z., Le T.T.;
 RA "The sequence of C. elegans esomid F47B3.8";
 RT Submitted (AF01147) to the EMBL/GenBank/DBJ databases.
 RN [3]
 PP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX Waterston R.;
 RA Submitted (AF01147) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U97017; AAB52363.1; -;
 DR HSSP: P01130; IAUJ.
 DR InterPro: IPR002106; AARNAL ligaseII.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000013; Ldl_receptor_1c4.
 DR InterPro: IPR003172; Ldl_receptor_A.
 DR Pfam: PF00057; ldl_receptor_11.
 DE Pfam: PF00059; ldl_receptor_2_9.
 DR PRINTS: PR00261; LDLRECEPTOR.
 DR SMART: SM00181; EGF; 4.
 DR SMART: SM00001; EGF-like; 1.
 DR SMART: SM0122; LDL3; 11.
 DR SMART: SM00135; LY; 15.
 DE Pfam: PF00119; AA_TERA_LIGASE_1; UNKNOWN 1.
 DP PROSITE: PS01186; EGF_2; UNKNOWN_2.
 DP PROSITE: PS01209; LDLRA_1; 9.
 DR PROSITE: PS00568; LDLRA_2; 11.
 KW Glycoprotein.
 SO SEQUENCE 2643 AA; 294294 MW; 550690A978CF20 CDS64;

Query Match 10.24; Score 79.5; DP 5; Length 2643;
 Best Local Similarity 24.28; Pred. No. 19;
 Matches 37; Conservative 15; Mismatches 34; Indels 63; Gaps 7;

Q1 40 GSEPTIHR-GYFQLEAVEFAEGRIFIAIEFASIDLEVLVILLI... 79
 D1 1596 GSNVSIIEVATQPSLIVHPSV-----FVIGDSGDSGFENELINNSNNHATQCT 1650
 Q2 80 -----VL-----VEGIDPNACHMVEFLVRLVYCTKTNWVFLAK 117
 D1 1651 NIGSTTTGCGVNIQQVILVATNGVPGSTDPHPHAPFVSGQYE-----NIEAVGSF 1705

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DR EMBL: AY071674; AAL49296.1; ...
DE Flyp130; Flyp0319601; CG1315.
DE InterPro: IPR03172; EI Def22 Def2.
DE Pfam: PF00221; EI Def22 Def2.1.
DE Pfam: PF00221; EI Def22 Def2.1.
DE SEQUENCE 157 AA; 1782 MW; 111FAAAGAAAGAAAGAAAG 75764;

Query Match 100% Score 297 EE 5; Length 157;
Seed Local Similarity: 24138; Field No. 13;
Matches 27; Conservation 19; Mismatch 10; Y-Rel 6; Gap

13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 10
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RT "The genome sequence of *Drosophila melanogaster*."

RL Genbank: 257.22185, 213512000)
 DR ENBL; AE003685; AAF54488.1; --
 DR FlyBase; FBgn0037742; CG12813
 DR InterPro; IPR001173; F1 DetP2 DefP2
 DR Pfam; PF02221; E1 DefP2 DefP2 1
 CC SEQUENCE 173 AA, 19640 MW, 458886BL4J3J3BL4 CR664;

Query Match 10.2%; Score 79; DB 5; Length 173;

Best Local Similarity 23.6%; Pred. No. 1.7;
 Matches 35; Conservative 21; Mismatches 40; Indels 12; Gaps 4;

QY 6 LALSLVAARQGVVFVTFANF--IPVVLVPTFDSRQCIHRYVFLLEAVFEANQM E3

DB 13 LLLSLAQAQPHQATEVYVCGKPPFLFVPHVCVTRFCQVKGTCQKPIDSAVDVY 71

QY 64 TETAFETETASIDG--LEVEFGIFMAVWVYHVFEEVLEYTMVVKIAP 114

DB 72 LLOHLVLAAILGLITVVELADVAACPVLQYAGCLPYTE--DVSYLTPPIGEY 129

QY 117 KLENVVTVKMGDGVLCACIATHAKI 144

DB 130 PEIGVKTIVLQDNEIATCFVTDIKV 157

RESULT 14

Q9SF20 PRELIMINARY; PRT; 153 AA.

AC Q9SF20;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE F26K24.7 protein (Hypothetical 16.9 kDa protein).

GN F26K24.7

OC Arabidopsis thaliana (Mouse ear cress)

OC Eukaryota, Viridiplantae, Euphyllophyta, Embryophyta, Tracheophyta

OC Spermatophyta, Gnuphyllales, Eudicotyledons, Core eudicots, Rosidae;

OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsis

OC NCBI_TaxID=1702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV, COLUMBIA;

PA Lin X., Kaul S., Town C.D., Penrice M., Creasy T.H., Haas B.

RA Renning C.W., Xie H., Fujii C.Y., Mottack T.P., Earnstead M.E.,

RA Rowan C.L., White O., Nierman W.C., Fraser C.M.;

RT "Arabidopsis thaliana chromosome III: PAC F25F74 genomic sequence."

RL Submitted (JAN 2001) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,

RA Bowser C., Gattinai P., Chen H., Cheuk P., Hayashizaki Y., Ishida J.,

RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,

RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,

RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,

RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

RT "Full Length cDNA of gene F26K24.7/Atg31780 (G16671934)."

RL Submitted (MAY 2001) to the EMBL/Genbank/DBJ databases.

DR ENBL; AC016795; AAF23194.1; --

DR ENBL; AY034906; AAK59413.1; --

KW Hypothetical protein.

SQ STUBNPF 154 AA, 16445 MW, E59C7AA41DEB09P CR664;

Query Match 10.2%; Score 78.5; DB 10; Length 153;

Best Local Similarity 24.5%; Pred. No. 1.6;

Matches 34; Conservative 22; Mismatches 40; Indels 43; Gaps 6;

QY 6 LCLSLVAARQGVVFVTFANF--IPVVLVPTFDSRQCIHRYVFLLEAVFEANQM E3

DB 16 LLLSLVAA-----TUVHLLDNNNEVYKQGV-DITPYPIARGEP----ATFRISANTD 65

QY 66 T----AKIEIKASIDGIVD-----VFSDPNACHYMKC 95

LL CC TEIDGDFVLEVSVDGWHHAFTHQVTFETVPAICHLVAAHGVLEHVFTHLRLRLM 125

QY 96 PLVWQQQVD---IKYTNV 111

DB 126 KMLDGRKVELTCKPSFDI 144

RESULT 15

Q98SS4 PRELIMINARY; PRT; 292 AA.

AC Q98SS4;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE ULIP4-like.

GN Gallus gallus (Chicken)

OC Eukaryota, Metazoa, Chordata, Clariata, Vertebrata, Euteleostomi;

OC Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;

OC Gallus.

OC NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE:21184110, PubMed:11087185,

PA Christianson J.H., Gyles F.G., Roberts V., Fajid A., Wilkinson D.G.;

PT "Screening from a subtracted embryonic chick hindbrain cDNA library:

RT identification of genes expressed during hindbrain, midbrain and

RL cranial neural crest development."

RL Mech. Dev. 102:119-133(2001).

DR ENBL; AF330010; AAK15320.1; --

DR InterPro; IPR002195; Dihydroorotase.

Pfam; PF00744; Dihydroorotase; 1.

SQ SEQUENCE 292 AA, 32115 MW, 51127:540E26CEB CR664;

Query Match 10.2%; Score 78.5; DB 13; Length 292;

Best Local Similarity 29.3%; Pred. No. 3.5;

Matches 34; Conservative 21; Mismatches 26; Indels 7; Gaps 1;

QY 2 MYFTCTGGLVAAVAPCVTVVTCDAHEHVLVFGHSEFCIHEGFTTLLAYPEAN 61

DB 181 MVEIFCIIPM/GAIAQVMAFNQDIEFPQPIIDIGITGPGHVLSPPEEVEASAVYPAI 240

QY 62 QNTKTA-----KIEIKASID 76

DB 243 TIAFANPLVYTFINGKPAD 262

Search Completed: March 10, 2003, 11:03:37

Job time : 35.4716 secs

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Result No.	Score		Query Match		Length	DB ID	Description
	Raw	Bit	Count	%			
1	773	100.0	146	14	AAP9160	Dermatophagoides p	
2	773	100.0	146	15	AAP51728	Der p II, Dermatop	
3	773	100.0	146	16	AAW1404	Der p I, Dermatop	
4	773	100.0	146	20	AAV50357	Dermatophagoides f	
5	773	100.0	146	20	AAV25581	Dermatophagoides s	
6	773	100.0	146	22	AAU11060	D. pteronyssinus a	
7	773	100.0	146	23	ABG67053	House dust mite al	
8	773	100.0	147	15	AAR37084	House dust mite al	
9	758	99.1	145	23	ABE76047	Protein allergen o	
10	755	97.7	145	21	ABP70485	House mite water al	
					AAP9160	Der p II antigen f	

PS Disclosure, Page 42, 12/9/99, English.

XX The cDNA encoding Dermatophagoides pteronyssinus Group II allergen
CC Dep pII was obtained in plasmid form as subclone from lambda gIII (Chua
CC et al., Int Arch Allergy Immun 119:123 (1999)). The cDNA was used to
CC express a Dep pII allergen capable of raising an immune response when
CC contacted with anti Dep pII antibodies. The protein was used to design
CC a series of overlapping peptides synthesized by standard techniques to
CC cover the whole Dermatophagoides pteronyssinus Dep pII sequence. The
CC cell epitopes of the protein were mapped by detection of the peptides
CC ability to stimulate T cell activity. The peptides may be used for
CC diagnosis and treatment of sensitivity to house dust mite allergens
CC When administered to house dust mite sensitive individuals, the
CC peptides are capable of modifying the allergic response to the
CC allergens. The peptides may be modified for e.g. increasing solubility,
CC enhancing therapeutic or preventive efficacy or stability.
XX See also MAP1994-030, MAP1994-031 and MAP1994-032

XX Sequence 146 AA.

Query Match 100.0%; Score 773; DP 14; Length 146;

Best Local Similarity 100.0%; Pred. No. 1.5e-85;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 MWYELLCSLLVAARQGVVVFETZARHEIFKVLVNGESENCTHPTFPAVFEFA 60

DB 1 MWYELLCSLLVAARQGVVVFETZARHEIFKVLVNGESENCTHPTFPAVFEFA 60

QY 61 NQNTTAKTEIFASISFSEFVTVVPGSDNACHVWTPPLVFGQGVFFYTWVVFAPFEN 120

DB 61 NQNTTAKTEIFASISFSEFVTVVPGSDNACHVWTPPLVFGQGVFFYTWVVFAPFEN 120

QY 121 VVTVVWMDGSGVLACAIATHAKIPD 146

DB 121 VVTVVWMDGSGVLACAIATHAKIPD 146

RESULT 2

AAAR51728

ID AAR51728 standard; Protein; 146 AA.

XX AAR51728;

AC AAR51728;

XX 01-FEB-1995 (first entry)

DT Der p II.

DE Group I; protein allergen; house dust mite; D. pteronyssinus; Der p I;

XX homolog; D. farinae; Der p I; Group II; Der p II; Der f II;

KW T-cell; epitopes; fusion peptides; antigenic fragments; substitution;

KW deletion; addition; chemical synthesis; antigenic fragments; substitution;

KW recombinant techniques; modify; allergic response; immunoglobulin E;

KW IGE; immunotherapy; IGE-mediated responses; anaphylaxis; tolerance;

KW anergise; T cell subpopulations; unresponsive; immune response;

XX lymphokine secretion profile.

XX Dermatophagoides pteronyssinus.

OS ZA9302677-A.

PN 26 JAN-1994.

XX 16-APR-1993; 93ZA-0002677.

PF 16-APR-1993; 93ZA-0002677.

XX (IMMU-) IMMULOGIC PHARM CORP.

PA Garman PD, Greenstein JL, Kuo M, Rogers RL;

XX WPI; 1994-128907/15.

XX N-PSDB; MAQ62109.

XX

PT Isolated and/or modified peptides comprising T-cell epitopes - of
PT major protein allergens of genus Dermatophagoides, used to treat
XX or diagnose sensitivity to house dust mites
XX Disclosure; Page 50-51; 154pp; English.

XX This sequence represents the group II protein allergen from the house
CC dust mite D. pteronyssinus, Der p II. The Der p II protein shows high
CC homology to the group II protein allergen derived from D. farinae, Der
CC f II, having an identity of 84%. Fragments of these proteins, and the
CC corresponding group I allergens, Der p I and Der f I, (see APP1991-941)
CC represent T-cell epitopes. Fusion peptides may be produced which
CC comprise at least two or three antigenic fragments. Each region of these
CC peptides may be derived from the same, or different, mite allergens. The
CC antigenic fragments may be altered by substitution, deletion or addition
CC to enhance their antigenicity. These peptides may be produced by
CC chemical synthesis, chemical cleavage of the fusion allergen or by
CC recombinant techniques. These peptides, when administered to a house
CC dust mite sensitive individual, are capable of modifying the allergic
CC response of the individual to the allergen. These peptides do not bind
CC to immunoglobulin E (IgE), or bind IgE to a lesser extent than the full
CC length protein allergen. This reduces the major complications of
CC standard immunotherapy, which are IGE-mediated responses such as
CC anaphylaxis. Exposure of mite allergic patients to these peptides may
CC relieve or avert severe allergic T cell subpopulations such that they
CC become unresponsive to mite allergens and do not participate in mounting
CC an immune response against the allergen. Administration of the peptides may
CC also modify the lymphokine secretion profile as compared with exposure
CC to the naturally occurring mite protein allergen.

XX Sequence 146 AA;

Query Match 100.0%; Score 773; DP 15; Length 146;

Best Local Similarity 100.0%; Pred. No. 1.5e-85;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWYELLCSLLVAARQGVVVFETZARHEIFKVLVNGESENCTHPTFPAVFEFA 60

DB 1 MWYELLCSLLVAARQGVVVFETZARHEIFKVLVNGESENCTHPTFPAVFEFA 60

QY 61 NQNTTAKTEIFASISFSEFVTVVPGSDNACHVWTPPLVFGQGVFFYTWVVFAPFEN 120

DB 61 NQNTTAKTEIFASISFSEFVTVVPGSDNACHVWTPPLVFGQGVFFYTWVVFAPFEN 120

QY 121 VVTVVWMDGSGVLACAIATHAKIPD 146

DB 121 VVTVVWMDGSGVLACAIATHAKIPD 146

RESULT 3

AAAW71909

ID AAW71909 standard; Protein; 146 AA.

XX AAW71909;

AC AAW71909;

XX 16-DEC-1998 (first entry)

DT Dermatophagoides Der p II.

DE Dermatophagoides Der p II.

XX Genus Dermatophagoides; major protein allergen; T cell epitopes;

KW Der p I, Der f II, Der f I, Der f II, Der f I, Der f II, Der f I, Der f II;

XX Dermatophagoides sp.

OS US5920862-A.

PN 13-OCT-1998.

XX 07-JUN-1998; 95US-0492142.

XX 15-MAY-1995; 95US-0445307.

XX 14-APR-1994; 94US-0227772.

XX 07 JUN 1995; 95US-0492142.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.
 PA Chen X, Evans S, Franzen HM, Garman RD, Greenstein JL;
 PI Kuo M, Rogers BL, Shaked Z,
 PY WPI: 1999-567530/48.
 DR N-PSDB; AAV611385.
 XX Dermatophagoides allergen peptides useful for treating house dust
 PT mite allergy
 PV Disclosure: Column 73-76; 155pp; English.
 YY The present invention describes peptides for treating sensitivity to
 CC house dust mite allergens from the genus Dermatophagoides. Peptides
 CC within the scope of the invention comprise at least one T cell epitope,
 CC or preferably at least two T cell epitopes of a protein allergen
 CC selected from the allergens Der p I, Der p II, Der f I, or Der f II.
 CC The invention also describes modified peptides having similar or
 CC enhanced therapeutic properties as the corresponding, naturally
 CC occurring allergen, but having reduced side effects. The present
 CC sequence represents Der p II from the present invention.
 XX
 SQ Sequence 146 AA;
 Query Match 100.0%; Score 773; DB 19; Length 146;
 Best Local Similarity 100.0%; Pred. No. 1.5e-85;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMYVHICLSLLVAAVAPQVNVVNCANHEIFVYVFGSGSEPCIIHQPFTELEAVPEA 60
 DB 1 MMYVHICLSLLVAAVAPQVNVVNCANHEIFVYVFGSGSEPCIIHQPFTELEAVPEA 60
 QY 61 NQNTTAFATFIFASIGLEVTVPSPICPNACHYMTFLVAAGVLIKFTINWVAIAPVSEN 120
 DB 61 NQNTTAFATFIFASIGLEVTVPSPICPNACHYMTFLVAAGVLIKFTINWVAIAPVSEN 120
 QY 121 VVTVKVMDDGVLACAIATHAKIRD 146
 DB 121 VVTVKVMDDGVLACAIATHAKIRD 146
 RESULT 4
 AAY50357
 ID AAY50357 standard; Protein: 146 AA.
 AC AAY50357;
 XX 26-JAN-2000 (first entry)
 DT Dermatophagoides sp. allergen Der p II protein.
 DE Allergen, house dust mite, detection, sensitivity; T cell epitope;
 KW screening; allergic disorder; asthma; rhinitis; eczema; dermatitis;
 KW Der p II.
 PY Dermatophagoides sp.
 OS US5968526-A.
 XX 19-OCT-1999.
 PD 07-JUN-1995; 95US-0478572.
 XX 19-MAY-1995; 95US-0445307.
 PP 14-APR-1994; 94US-0227772.
 PP 12-APR-1995; 95WO-0504461.
 XX (IMMU-) IMMUNOLOGIC PHARM CORP.
 PA Garman RD, Greenstein JL, Rogers BL, Franzen HM, Shaked Z, Chen X,
 PI Evans S, Kuo M;

XX WPI: 1999-590385/50.
 DR N-PSDB; AAZ233007.
 XX Screening individuals for allergic reactions to T cell epitopes of
 PT major allergens from house dust mites
 XX Disclosure: Column 75-78; 158pp; English.
 XX This invention describes a novel method (I) for detecting whether an
 CC individual is sensitive to Dermatophagoides (house dust mites). The
 CC method involves detecting sensitivity to house dust mites in patients,
 CC comprising combining a blood sample from the individual with 1 or more
 CC isolated T cell epitopes of the protein allergens I and II (DP I) and
 CC (DP II) from Dermatophagoides (house dust mites). 32 T cell epitopes
 CC with varying, defined minor acid sequences (given in the specification)
 CC may be used in (I). The sample and allergens are combined under
 CC conditions appropriate for the binding of T cell epitopes with the
 CC polypeptides. The extent of binding is then indicative of the sensitivity
 CC of the patient to house dust mites. (I) may be used to screen individuals
 CC for sensitivity to Dermatophagoides (house dust mites). The house dust
 CC mite is a major cause of a variety of allergic disorders such as asthma,
 CC rhinitis and eczema/dermatitis. This sequence represents the house dust
 CC mite allergen Der p II.
 XX
 SQ Sequence 146 AA;
 Query Match 100.0%; Score 773; DB 20; Length 146;
 Best Local Similarity 100.0%; Pred. No. 1.5e-85;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMYVHICLSLLVAAVAPQVNVVNCANHEIFVYVFGSGSEPCIIHQPFTELEAVPEA 60
 DB 1 MMYVHICLSLLVAAVAPQVNVVNCANHEIFVYVFGSGSEPCIIHQPFTELEAVPEA 60
 QY 61 NQNTTAFATFIFASIGLEVTVPSPICPNACHYMTFLVAAGVLIKFTINWVAIAPVSEN 120
 DB 61 NQNTTAFATFIFASIGLEVTVPSPICPNACHYMTFLVAAGVLIKFTINWVAIAPVSEN 120
 QY 121 VVTVKVMDDGVLACAIATHAKIRD 146
 DB 121 VVTVKVMDDGVLACAIATHAKIRD 146
 RESULT 5
 AAY25581
 ID AAY25581 standard; Protein: 146 AA.
 AC AAY25581;
 XX 30-SEP-1999 (first entry)
 DT D. pteronyssinus allergen Der p 2 protein fragment.
 DE Major histocompatibility complex, class II, desmodiosin, human;
 KW allergen, grass, tree, weed, pollen, fungi, mould, food, insect, sting;
 KW chironomidae, spider, mite; housefly, fruit fly, sheep blow fly, honeybee;
 KW screw worm fly; grain weevil; silkworm; bee moth; larva; mealworm; cat;
 KW cockroach, beetle, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig;
 KW mice, gerbil; vaccine; treatment; prevention; hypersensitivity.
 XX Dermatophagoides pteronyssinus.
 OS WO9934826-A1.
 XX 15-JUL-1999.
 PD 11-JAN-1999; 99WO-0800080.
 XX 21-SEP-1998; 98EP-0070474.
 PP 09-JAN-1999; 98EP-0000445.
 XX (IMMU-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA

16 NOV-2000; 200005-249451P.
14 JUN-2001; 200105-238170P.

(ALKA-) ALK ABELLO AS.

Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD.

WP1; 2002-508328/54.

N-PSDB; ABE95700.

New recombinant mutant allergen, useful for preventing and/or treating allergy, comprises multiple mutations and reduced immunoglobulin E binding affinity.

Claim 60; Fig 16; 210pp; English.

The invention relates to a recombinant allergen (I) which is a mutant of a naturally occurring allergen, where the mutant allergen has at least four primary mutations, which each reduce the specific immunoglobulin E (IgE) binding capability of the mutant allergen as compared to the IgE binding capability of the naturally occurring allergen, where each primary mutation is a substitution of one surface-exposed amino acid residue with another residue, which does not occur in the same position in the amino acid sequence of any known homologous protein within the taxonomic species from which the naturally occurring allergen originates, and each primary mutation is spaced from each other primary mutation by at least 15 Angstrom, and the primary mutations are placed in such a manner that at least one circular surface region with a area of 800 Angstrom² comprises no mutation. Also included are a composition comprising two or more of the recombinant allergens, where the variant allergen is defined by having at least one primary mutation, which is absent in at least one of the other variants, and for each variant no secondary mutation is present within a radius of 15 Angstrom from each absent primary mutation; a DNA sequence encoding the recombinant allergen or its derivative, partial sequence or degenerated sequence, or a sequence which hybridises to it under stringent conditions, where the derivative, partial sequence, degenerated sequence or hybridising sequence encodes a peptide having at least one B cell epitope; an expression vector comprising the DNA and a host cell comprising the vector. The recombinant allergen is useful as a pharmaceutical, for preparing a pharmaceutical for preventing and/or treating allergy, or in a diagnostic assay for assessing relevance, safety or outcome of therapy, of a subject, where an IgE containing sample of the subject is mixed with the recombinant allergen and assessed for the level of reactivity between the IgE in the sample and the recombinant allergen. The recombinant allergen or compositions are useful for generating an immune response in a subject, for vaccination or treatment of a subject or for the treatment, prevention or alleviation of allergic reactions in a subject, e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or systemic anaphylactic reactions. The present sequence represents a wild type allergen of the invention.

Sequence 146 AA;

Query Match 100.0%; Score 773; DB 23; Length 146;
Best Local Similarity 100.0%; Field No.: 50-85;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVFILCLSLVAAPVQGVVVFVTCANHFIPVLPVPCGCHSEPCIIHPGKFFQLEAVFEA 60

Db 1 MMVFILCLSLVAAPVQGVVVFVTCANHFIPVLPVPCGCHSEPCIIHPGKFFQLEAVFEA 60

QY 61 NONTKTAFITFKASIDGLEVEVPSIGFNACHYKPTLVFQDQYDIFYWVWVKYIAFKSEN 120

Db 61 NONTKTAFITFKASIDGLEVEVPSIGFNACHYKPTLVFQDQYDIFYWVWVKYIAFKSEN 120

QY 121 VVTVKVMGDDGVLCACIAATHAKIRD 146

Db 121 VVTVKVMGDDGVLCACIAATHAKIRD 146

RESULT 8
AAP47064

ID AAR47064 standard, Protein; 147 AA.

AC AAR47064;

XX 17-OCT-1994 (first entry)

XX Protein allergen of Derp II.

XX Der pII; House Dust Mite Allergen; ss.

XX Permatrophagoides pteronyssinus.

XX Key Location/Qualifiers
FH Peptide 2..17

FT /label= signal peptide
FT /note= "typical sequence with a hydrophobic core"

FT Protein 18..146
FT /label= Der pII

XX WC9405790-A.

XX 17-MAR-1994.

XX 10 SEP-1993; 93WO-0588518.

XX 10 SEP-1993; 93WO-0588518.

XX (IMMU-) IMMULOGIC PHARM CORP.

XX Chua K, Thomas WR;

XX WFI; 1994-101195/12.

XX N-PSDB; AAQ58666.

XX New protein allergens of house dust mite used for diagnosing PT and treating sensitivity in an individual to house dust mite PT allergens

XX Example 5, Fig 7, 9pp; English.

XX The sequence shows unprocessed Der pII with a normal signal CC peptide. The mature protein can be used to test sensitivity in CC an individual to house dust mite and to reduce the sensitivity of CC the individual.

XX Sequence 147 AA;

Query Match 100.0%; Score 773; DB 15; Length 147;

Best Local Similarity 100.0%; Field No.: 50-85;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVFILCLSLVAAPVQGVVVFVTCANHFIPVLPVPCGCHSEPCIIHPGKFFQLEAVFEA 60

Db 1 MMVFILCLSLVAAPVQGVVVFVTCANHFIPVLPVPCGCHSEPCIIHPGKFFQLEAVFEA 60

QY 61 NONTKTAFITFKASIDGLEVEVPSIGFNACHYKPTLVFQDQYDIFYWVWVKYIAFKSEN 120

Db 61 NONTKTAFITFKASIDGLEVEVPSIGFNACHYKPTLVFQDQYDIFYWVWVKYIAFKSEN 120

QY 121 VVTVKVMGDDGVLCACIAATHAKIRD 146

Db 121 VVTVKVMGDDGVLCACIAATHAKIRD 146

RESULT 9

ABB76047

ID ABB76047 standard, Protein; 145 AA.

XX ABB76047;

XX 12 JUL 2002 (first entry)

XX Dust mite major allergen Der p 2.

RESULT 11

ABG66997
ID ABG66997 standard; Protein; 129 AA.

XX AC ABG66997;
XX AA

XX DT 24 SEP 2002 (first entry)
XX

XX Query first mice allergen Der p 2 ALK-114.
XX

XX Immunoglobulin E, IgE, allergen, allergy, hay fever;
XX rhinoconjunctivitis, rhinitis, asthma, systemic anaphylaxis;
XX vaccine, antiallergic, B cell epitope.
XX

XX Dermatophagoides pteronyssinus.
XX

XX WC2002040676-A2.
XX

XX 23 MAY-2002.
XX

XX 16 NOV 2001; 2001WU-DK00764.
XX

XX 16-NOV-2000; 2000UK-0001718
XX

XX 14 JUN-2001; 2001US-298170P.
XX

XX (ALKA-) ALK-ABELLO AS.
XX

XX Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX

XX WPI; 2002-508328/54.
XX

XX N-PSUR; AR64475.
XX

XX New recombinant mutant allergen, useful for preventing and/or treating
XX allergy, comprises multiple mutations and reduced immunoglobulin E
XX binding affinity
XX

XX Example 5; Page 93; 210pp; English.
XX

XX The invention relates to a recombinant allergen (I) which is a mutant of
XX a naturally occurring allergen, where the mutant allergen has at least
XX four primary mutations, which each reduce the specific immunoglobulin E
XX (IgE) binding capability of the mutant allergen as compared to the IgE
XX binding capability of the naturally occurring allergen, where each
XX primary mutation is a substitution of one surface exposed amino acid
XX residue with another residue, which does not occur in the same position
XX in the amino acid sequence of any known homologous protein within the
XX taxonomic species from which the naturally occurring allergen
XX originates, and each primary mutation is spaced from each other primary
XX mutation by at least 15 Angstrom, and the primary mutations are placed
XX in such a manner that at least one circular surface region with a area
XX of 800 Angstrom² comprises no mutation. Also included are a composition
XX comprising two or more of the recombinant allergens, where the variant
XX allergen is defined by having at least one primary mutation, which is
XX absent in at least one of the other variants, and for each variant no
XX secondary mutation is present within a radius of 15 Angstrom from each
XX absent primary mutation; a DNA sequence encoding the recombinant allergen
XX or its derivative, partial sequence or degenerated sequence, or a
XX sequence which hybridises to it under stringent conditions, where the
XX derivative, partial sequence, degenerated sequence or hybridising
XX sequence encodes a peptide having at least one B cell epitope; an
XX expression vector comprising the DNA and a host cell comprising the
XX vector. The recombinant allergen is useful as a pharmaceutical, for
XX preparing a pharmaceutical for preventing and/or treating allergy, or in
XX a diagnostic assay for assessing relevance, safety or outcome of therapy
XX of a subject, where an IgE containing sample of the subject is mixed
XX with the recombinant allergen and assessed for the level of reactivity
XX between the IgE in the sample and the recombinant allergen. The
XX recombinant allergen or compositions are useful for generating an
XX immune response in a subject, for vaccination or treatment of a subject
XX or for the treatment, prevention or alleviation of allergic reactions
XX in a subject e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or
XX systemic anaphylaxis. The present application represents a full range

CC allergen of the invention.

XX SQ Sequence 129 AA;
XX

XX Query Match 89.7%; Score 693; DB 23; Length 129;
XX Best Local Similarity 100.0%; Field No. 6.6e-76;
XX Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 18 EQVLYVTACHIEIFFVLMVSESESEIETTHHSPFQSLZAKFEAGLRTKTAIEKASLIG 77
XX 1 EQVDVWTACHIEIFFVLMVSESESEIETTHHSPFQSLZAKFEAGLRTKTAIEKASLIG 60

XX 78 LEVTVFSTFSTNA THVMWTEIYVQGLLITITVYTHWQFIATFSENVTWVWVWDESVLACA 137
XX 1 LEVTVFSTFSTNA THVMWTEIYVQGLLITITVYTHWQFIATFSENVTWVWVWDESVLACA 120

XX 138 IATHAKIRD 146
XX 121 IATHAKIRD 129

XX RESULT 12
XX ABG67001

XX 12 APG67001 standard; Protein; 129 AA.
XX

XX AC ABG67001;
XX

XX 24 SEP 2002 (first entry)
XX

XX House dust mite allergen Der p 2 ALK 114 mutant S24N.
XX

XX Immunoglobulin E, IgE, allergen, allergy, murine, hay fever;
XX rhinoconjunctivitis, rhinitis, asthma, systemic anaphylaxis; mutant;
XX vaccine, antiallergic, B cell epitope.
XX

XX Dermatophagoides pteronyssinus.
XX

XX Synthetic.
XX

XX WC2002040676-A2.
XX

XX 23 MAY 2002.
XX

XX 16 NOV 2001; 2001WE DKS3754.
XX

XX 16-NOV-2000; 2000UK 0001719.
XX

XX 14 JUN 2001; 2001US 249361P.
XX

XX (ALKA-) ALK-ABELLO AS.
XX

XX Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX

XX WPI; 2002-508328/54.
XX

XX New recombinant mutant allergen, useful for preventing and/or treating
XX allergy, comprises multiple mutations and reduced immunoglobulin E
XX binding affinity -
XX

XX Example 6; Page 210pp; English.
XX

XX The invention relates to a recombinant allergen (I) which is a mutant of
XX a naturally occurring allergen, where the mutant allergen has at least
XX four primary mutations, which each reduce the specific immunoglobulin E
XX (IgE) binding capability of the mutant allergen as compared to the IgE
XX binding capability of the naturally occurring allergen, where each
XX primary mutation is a substitution of one surface-exposed amino acid
XX residue with another residue, which does not occur in the same position
XX in the amino acid sequence of any known homologous protein within the
XX taxonomic species from which the naturally occurring allergen
XX originates, and each primary mutation is spaced from each other primary
XX mutation by at least 15 Angstrom, and the primary mutations are placed
XX in such a manner that at least one circular surface region with a area
XX of 800 Angstrom² comprises no mutation. Also included are a composition

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; APPLICANT: CONSIGLIO NAZIONALE DELLE PIROPICHE
; TITLE OF INVENTION: VARIANTS OF ALLERGENIC PROTEINS OF THE GROUP 2 OF
; FILE REFERENCE: DERMATOPHAGOIDES
; CURRENT APPLICATION NUMBER: US/09/949,889
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Dermatophagoides pteromyssinus
US-09-949-889-3

Query Match      94.5%; Score 653; DP 10; Length 129;
Best Local Similarity 94.6%; Pred. No. 5,2e-67;
Matches 122; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cj 1 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 61
Db 1 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 61

Cj 2 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 121
Db 2 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 121

Cj 3 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 145
Db 3 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 145

RESULT 3
UC-09-949-889-3
; Sequence 4, Application US/09949889
; Patent No. US20020054881A1
; GENERAL INFORMATION:
; APPLICANT: CONSIGLIO NAZIONALE DELLE PIROPICHE
; TITLE OF INVENTION: VARIANTS OF ALLERGENIC PROTEINS OF THE GROUP 2 OF
; FILE REFERENCE: DERMATOPHAGOIDES
; CURRENT APPLICATION NUMBER: US/09/949,889
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Dermatophagoides pteromyssinus
US-09-949-889-4

Query Match      94.5%; Score 653; DP 10; Length 129;
Best Local Similarity 94.6%; Pred. No. 5,2e-67;
Matches 122; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cj 1 DOVYVDCARHEIKVAVGCHCEPFIHFKFFLEAFVFA 77
Db 1 DOVYVDCARHEIKVAVGCHCEPFIHFKFFLEAFVFA 77

Cj 2 DOVYVDCARHEIKVAVGCHCEPFIHFKFFLEAFVFA 127
Db 2 DOVYVDCARHEIKVAVGCHCEPFIHFKFFLEAFVFA 127

Cj 3 DOVYVDCARHEIKVAVGCHCEPFIHFKFFLEAFVFA 145
Db 3 DOVYVDCARHEIKVAVGCHCEPFIHFKFFLEAFVFA 145

Query Match      94.5%; Score 653; DP 10; Length 129;
Best Local Similarity 94.6%; Pred. No. 5,2e-67;
Matches 122; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cj 1 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 61
Db 1 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 61

Cj 2 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 121
Db 2 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 121

Cj 3 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 145
Db 3 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 145

RESULT 4
US-09-860-793-3
; Sequence 3, Application US/09860793
; Patent No. US20020136734A1
; GENERAL INFORMATION:
; APPLICANT: Temeeyer, Kevin B
; TITLE OF INVENTION: Vaccines for the Protection of Cattle from Bacteriophagic
; FILE REFERENCE: Docket 0047 96 - John H. Pruett et al.
; CURRENT APPLICATION NUMBER: US/09/860,793
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Proteus ovis
US-09-860-793-3

Query Match      36.7%; Score 281.5; DP 10; Length 143;
Best Local Similarity 38.3%; Pred. No. 5,7e-25;
Matches 49; Conservative 37; Mismatches 39; Indels 3; Gaps 3;

Cj 1 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 61
Db 1 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 61

Cj 2 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 121
Db 2 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 121

Cj 3 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 143
Db 3 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 143

RESULT 5
US-09-860-793-1
; Sequence 1, Application US/09860793
; Patent No. US20020136734A1
; GENERAL INFORMATION:
; APPLICANT: Pruett, John H
; TITLE OF INVENTION: Vaccines for the Protection of Cattle from Bacteriophagic
; FILE REFERENCE: Docket 0047 96 - John H. Pruett et al.
; CURRENT APPLICATION NUMBER: US/09/860,793
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/366,603
; PRIOR FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Proteus ovis
; FEATURE:
; NAME/KEY: VAPIANT
; LOCATION: (1)
; OTHER INFORMATION: Y at position 1 may also be C or S or V
US-09-860-793-1

Query Match      36.7%; Score 281.5; DP 10; Length 143;
Best Local Similarity 38.3%; Pred. No. 5,7e-25;
Matches 49; Conservative 37; Mismatches 39; Indels 3; Gaps 3;

Cj 1 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 61
Db 1 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 61

Cj 2 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 121
Db 2 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 121

Cj 3 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 143
Db 3 MYKILSLVAVARQVVEGCAHEIFVAVGCHCEPFIHFKFFLEAFVFA 143

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; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaValle, Edward P.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SCRYPTED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; EARLIER FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 168
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: UNSURE
; LOCATION: (95)
; US-10-114-893-168

Query Match 15.5%; Score 119.5; DB 9; Length 149;
Best Local Similarity 26.8%; Pred No 4 9a-05;
Matches 34; Conservative 30; Mismatches 55; Indels 13; Gaps 5;

QY 6 LCTSLVAAVAPDVVDFQCANH...EIPVVLVPGCHGSEPCIIHGKPPQLKAVPEANON 63
DB 8 ILLALVAASQAEPLHFDGSKGVIVKVNVSQC-PTDPCQLHKQGSYVAITTSQTQ 66
QY 64 TTKAKIRIKASIDLEVDVPGCIDNACHY-MKCPVLVGGQYDIDKYTWNVKPIAPSE--- 119
DB 67 SQNTALVHGILPGIPVPPFPIEDPGYGGINGITQDKYSY.....INKLVNREYPS 121
QY 120 -NVVTVVWMT 130
DB 122 IKLVVWVLEDD 133

RESULT 10
US-10-040-916-45
; Sequence 45 Application US/10/114,893
; Patent No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: LaValle, Edward
; APPLICANT: Racie, Lisa
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Evans, Cheryl
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SCRYPTED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 47 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaValle, Edward P.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SCRYPTED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; EARLIER FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 168
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: UNSURE
; LOCATION: (95)
; US-10-114-893-168

Query Match 15.5%; Score 119.5; DB 9; Length 149;
Best Local Similarity 26.8%; Pred No 4 9a-05;
Matches 34; Conservative 30; Mismatches 55; Indels 13; Gaps 5;

QY 6 LCTSLVAAVAPDVVDFQCANH...EIPVVLVPGCHGSEPCIIHGKPPQLKAVPEANON 63
DB 8 ILLALVAASQAEPLHFDGSKGVIVKVNVSQC-PTDPCQLHKQGSYVAITTSQTQ 66
QY 64 TTKAKIRIKASIDLEVDVPGCIDNACHY-MKCPVLVGGQYDIDKYTWNVKPIAPSE--- 119
DB 67 SQNTALVHGILPGIPVPPFPIEDPGYGGINGITQDKYSY.....INKLVNREYPS 121
QY 120 -NVVTVVWMT 130
DB 122 IKLVVWVLEDD 133

RESULT 10
US-10-040-916-45
; Sequence 45 Application US/10/114,893
; Patent No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: LaValle, Edward
; APPLICANT: Racie, Lisa
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Evans, Cheryl
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SCRYPTED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 47 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,916
FILING DATE: 07 Jan 2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/837,029
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: 08/686,878
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-040-916-45

Query Match 14.0%; Score 108.5; DB 12; Length 120;
Best Local Similarity 26.8%; Pred No 4 9a-05;
Matches 31; Conservative 26; Mismatches 51; Indels 9; Gaps 5;

QY 5 LCTSLVAAVAPDVVDFQCANH...EIPVVLVPGCHGSEPCIIHGKPPQLKAVPEANON 63
DB 8 ILLALVAASQAEPLHFDGSKGVIVKVNVSQC-PTDPCQLHKQGSYVAITTSQTQ 66
QY 64 TTKAKIRIKASIDLEVDVPGCIDNACHY-MKCPVLVGGQYDIDKYTWNVKPIAPSE 119
DB 67 SQNTALVHGILPGIPVPPFPIEDPGYGGINGITQDKYSY.....INKLVNREYPS 118

RESULT 11
US-09-860-793-7
; Sequence 7 Application US/09/860,793
; Patent No. US20020136734A1
; GENERAL INFORMATION:
; APPLICANT: Pruett, John H.
; APPLICANT: Temeyer, Kevin B.
; APPLICANT: Kunz, Sidney E.
; APPLICANT: Fisher, William F.
; TITLE OF INVENTION: Vaccines for the Prevention of Cancer from Peptidic
; TITLE OF INVENTION: Scabies
; FILE REFERENCE: Docket 004/96; John H. Pruett et al.
; CURRENT APPLICATION NUMBER: US/09/860,793
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/365,603
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
; US-09-860-793-7

Query Match 13.8%; Score 107; DB 10; Length 22;
Best Local Similarity 26.4%; Pred No 7 1a-06;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 19 QVIVKDCANHEIKYVLVPGCHG 40
DB 1 QVIVKDCANHEIKYVLVPGCHG 22

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Q7	1	MMKFTLHCSTLVAAVAPQVNVPCANETIKYVLVDSHSEPCIIHSPCTFLEAVEA	60
Db	1	MMKFTLHCSTLVAAVAPQVNVPCANETIKYVLVDSHSEPCIIHSPCTFLEAVEA	60
Q7	61	NQNTTAPITFISAGTGLELVNVPGLDPSACHVYVPTLVKQCCQYIKVWNVPTIADCPN	120
Db	61	NQNTTAPITFISAGTGLELVNVPGLDPSACHVYVPTLVKQCCQYIKVWNVPTIADCPN	120
Q7	121	VVVTVMVGQDGLACAIATKATP	146
Db	121	VVVTVMVGQDGLACAIATKATP	146

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1  RESULT 2
2  US-08-462-831-4
3  : Sequence 4, Application US/08462831
4  : Patent No. 5552142
5  : GENERAL INFORMATION:
6  : APPLICANT:
7  : TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
8  : TITLE OF INVENTION: DEPMATHEASITIPS
9  : NUMBER OF SEQUENCES: 13
10 : CORRESPONDENCE ADDRESS:
11 : ADDRESS: 14141V & COFFFIELD
12 : STREET: 60 STATE STREET, SUITE 510
13 : CITY: BOSTON
14 : STATE: MA
15 : COUNTRY: USA
16 : ZIP: 02109
17 : COMPUTER READABLE FORM:
18 : MEDIUM TYPE: FLOPPY disk
19 : COMPUTER: IBM PC compatible
20 : OPERATING SYSTEM: PC-DOS/MS-DOS
21 : SOFTWARE: ASCII TEXT
22 : CURRENT APPLICATION DATA:
23 : APPLICATION NUMBER: US/08/462, 831
24 : FILING DATE:
25 : CLASSIFICATION: 424
26 : PRIORITY APPLICATION DATA:
27 : APPLICATION NUMBER: US 07/945, 588
28 : FILING DATE: 10 SEPTEMBER 1997
29 : APPLICATION NUMBER: US 580, 555
30 : FILING DATE: 11 SEPTEMBER 1990
31 : APPLICATION NUMBER: US 459, 642
32 : FILING DATE: 13 FEBRUARY 1990
33 : ATTORNEY/AGENT INFORMATION:
34 : NAME: MANDRAGOURAS, AMY E.
35 : REGISTRATION NUMBER: 36,207
36 : REFERENCE/PRIORITY NUMBER: IPC 010CC (JWI 024)
37 : TELECOMMUNICATION INFORMATION:
38 : TELEPHONE: (617) 227-7400
39 : TELEFAX: (617) 227-5941
40 : INFORMATION FOR SEQ ID NO: 4:
41 : SEQUENCE CHARACTERISTICS:
42 : LENGTH: 146 amino acids
43 : TYPE: crims acid
44 : TOPOLOGY: linear
45 : MOLECULE TYPE: Protein
46 : US-08-462-831-4

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Db 121 VVVVWMMDDCVLACAIATHAXIPD 146

|||||

RESULT 3
US-08-461-809-4
S-P-N = 4; Application No. US/9451279
Patent No. 5770202
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ANTIGENOS FROM
TITLE OF INVENTION: DEPMATOPHAGOCIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COOYFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/05/451,809
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 880,688
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: WANDEGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
PREFERRED/CORRET NAMEPP: P.C.O.C.C.C (INV. 024)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-809-4

RESULT 4
 US-08-461-441-4
 ; S. 100-461-441-4
 ; Patent No. 5773002
 ; GENERAL INFORMATION:


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1 TELEPHONE: (617) 227-7400
2 TELEFAX: (617) 227-5941
3 INFORMATION FOR SEQ ID NO: 4:
4 SEQUENCE CHARACTERISTICS:
5 LENGTH: 146 amino acids
6 TYPE: amino acid
7 TOPOLOGY: linear
8 MOLECULE TYPE: protein
9 PRT CD3 89218 4
10
11 Query Match 100.00, Score 773.10, E-Value 1.45e-145
12 Best Local Similarity 100.00, Prod No. 7.2e-99
13 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps
14
15 QY 1 MMYKYLQGLVAAYAFQYVWGTAMHIEIVLWPGGTHSEFTHREHFFLELVFEA 60
16 DB 1 MMYKYLQGLVAAYAFQYVWGTAMHIEIVLWPGGTHSEFTHREHFFLELVFEA 60
17
18 QY 61 NQNTAKIEIKATSEVVFTHSEFENACHMCKPLVLRGGVDYKVTWVPIAPSEN 120
19 DB 61 NQNTAKIEIKATSEVVFTHSEFENACHMCKPLVLRGGVDYKVTWVPIAPSEN 120
20
21 QY 121 VVTVKVMGGDGYLACAIATHAKIRD 146
22 DB 121 VVTVKVMGGDGYLACAIATHAKIRD 146
23
24 RESULT 9
25 US:08 460-040-6
26 : Sequence 6, Application US:08460040
27 : Patent No. 6071522
28 : GENERAL INFORMATION:
29 : APPLICANT: Thomas, Wayne R.
30 : TITLE OF INVENTION: Cloning of Mite Allergens
31 : NUMBER OF SEQUENCES: 8
32 : CORRESPONDENT ADDRESS:
33 : ADDRESSEE: LAHIVE & COCKFIELD
34 : STREET: 60 State Street, Suite 510
35 : CITY: Boston
36 : STATE: Massachusetts
37 : COUNTRY: USA
38 : ZIP: 02109-1075
39 : COMPUTER READABLE FORM:
40 : MEDIUM TYPE: floppy disk
41 : COMPUTER: IBM PC compatible
42 : OPERATING SYSTEM: PC DOS/MS-DOS
43 : SOFTWARE: Patent in Release #1.0, Version #1.25
44 : CURRENT APPLICATION DATA:
45 : APPLICATION NUMBER: US:08/460,040
46 : FILING DATE: 2-JUNE-95
47 : CLASSIFICATION: 435
48 : PRIOR APPLICATION DATA:
49 : APPLICATION NUMBER: 08/460,722
50 : FILING DATE: 8-NOV-93
51 : APPLICATION NUMBER: 07/458,542
52 : FILING DATE: 13-FEB-90
53 : APPLICATION NUMBER: PCT/AU98/00195
54 : FILING DATE: 17-JUNE-88
55 : APPLICATION NUMBER: PI 2523/87
56 : FILING DATE: 18-JUNE-87
57 : ATTORNEY/AGENT INFORMATION:
58 : NAME: Amy E. Mandragouras
59 : REGISTRATION NUMBER: 36,207
60 : REFERENCE/DOCVET NUMBER: IMI-0210N2
61 : TELECOMMUNICATION INFORMATION:
62 : TELEPHONE: (617)227-7400
63 : TELEFAX: (617)227-5941
64 : INFORMATION FOR SEQ ID NO: 6:
65 : SEQUENCE CHARACTERISTICS:
66 : LENGTH: 145 amino acids
67 : TYPE: amino acid
68 : TOPOLOGY: linear
69 : MOLECULE TYPE: protein

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FEATURE:
NAME/KEY: misc feature
LOCATION: 47
OTHER INFORMATION: /label-xaa is Thr or Ser
FEATURE:
NAME/KEY: misc feature
LOCATION: 114
OTHER INFORMATION: /label-xaa is Asp or Asn
FEATURE:
NAME/KEY: misc feature
LOCATION: 127
OTHER INFORMATION: /label-xaa is Ile or Leu
US 08-461 809-12
Query Match
Best Local Similarity 97.5%; Score 676; DB 1; Length 129;
Matches 126; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 18 DOVDVFTCAHIEFFVIVVSTHSEPTIIRHSGFLEAVSEANENHIAHIEIPASING 77
Db 1 DOVDVFTCAHIEFFVIVVSTHSEPTIIRHSGFLEAVSEANENHIAHIEIPASING 60
QY 78 LEVDVFGIDPNACHYKCPDLVKGQGVQVQVIVYVWVVPKADPSNNVYVVMGDCGVLA 137
Db 61 LEVDVFGIDPNACHYKCPDLVKGQGVQVQVIVYVWVVPKADPSNNVYVVMGDCGVLA 120
QY 138 IATHAKIRD 146
Db 121 IATHAKIRD 129
RESULT 13
US-08-461-441-12
Sequence 12, Application US/08461441
Patent No. 5773002
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: 1 CELL EPITOPES OF THE MAJOR ALLERGENS FROM
TITLE OF INVENTION: DERMATOPHAGOIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,441
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
APPLICATION NUMBER: US 580,455
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-0100C (IMI-024)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
NAME/KEY: misc feature
LOCATION: 47
FEATURE:
NAME/KEY: misc feature
LOCATION: 47
OTHER INFORMATION: /label-xaa is Thr or Ser
FEATURE:
NAME/KEY: misc feature
LOCATION: 114
OTHER INFORMATION: /label-xaa is Asp or Asn
FEATURE:
NAME/KEY: misc feature
LOCATION: 127
OTHER INFORMATION: /label-xaa is Ile or Leu
US 08-461 809-12
Query Match
Best Local Similarity 97.7%; Score 676; DB 1; Length 129;
Matches 126; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 18 DOVDVFTCAHIEFFVIVVSTHSEPTIIRHSGFLEAVSEANENHIAHIEIPASING 77
Db 1 DOVDVFTCAHIEFFVIVVSTHSEPTIIRHSGFLEAVSEANENHIAHIEIPASING 60
QY 78 LEVDVFGIDPNACHYKCPDLVKGQGVQVQVIVYVWVVPKADPSNNVYVVMGDCGVLA 137
Db 61 LEVDVFGIDPNACHYKCPDLVKGQGVQVQVIVYVWVVPKADPSNNVYVVMGDCGVLA 120
QY 138 IATHAKIRD 146
Db 121 IATHAKIRD 129
RESULT 14
PCT-US93-08518-12
Sequence 12, Application PCT/US93/08518
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: 1 CELL EPITOPES OF THE MAJOR ALLERGENS FROM
TITLE OF INVENTION: DERMATOPHAGOIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08518
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: 10 SEPTEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-0100C (IMI-024)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
NAME/KEY: misc feature
LOCATION: 47
FEATURE:
```


GenCore version 1.4.10.1004
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OM protein protein search, using sw model

Run on: March 11, 2003, 15:23:44, Search time 18.552 Seconds
(without alignments)
326.361 Million cell updates/sec

Title: US-09-877-160.3

Perfect score: 773
Sequence: 1 MMVKITLSTSLVAARVAPGV.....VMSSGVLCALATHAKIED 146

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112992 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112992

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	773	100	0	1 ALL2 DERPPT	P49278 Dermaphag
2	687	88.9	146	1 ALL2 DERFA	Q04851 Dermaphag
3	676	87.5	145	1 ALL2 DERMA	Q04822 Dermaphag
4	290.5	37.6	141	1 ALL2 YPPPT	Q03800 Dermaphag
5	278.5	36.0	141	1 ALL2 DERPC	P80384 Dermaphag
6	135.5	17.5	149	1 NPC2 EPG	Q07763 Dermaphag
7	127.5	16.5	149	1 NPC2 BOVIN	P79345 Dermaphag
8	126.5	16.4	148	1 NPC2 BOVIN	Q07452 Dermaphag
9	123	15.9	151	1 NPC2 HUMAN	Q15608 Dermaphag
10	118.5	15.3	149	1 NPC2 MOUSE	Q02098 Dermaphag
11	112	14.5	149	1 NPC2 BRARE	Q04933 Dermaphag
12	105	13.6	149	1 NPC2 CANFA	Q08895 Dermaphag
13	90.5	11.7	145	1 ES16 MANSP	Q25491 Dermaphag
14	89	11.5	151	1 YG27 METJA	Q59021 Dermaphag
15	86.5	11.2	577	1 ITB6 CAVPO	P18563 Dermaphag
16	79.5	10.3	788	1 ITB6 HUMAN	P18564 Dermaphag
17	79	10.2	255	1 NPC1 HUMAN	P46331 Dermaphag
18	76	9.8	175	1 DEST MYXXA	P02967 Dermaphag
19	74.5	9.6	324	1 CATV NPVOP	Q10364 Dermaphag
20	73.5	9.5	2109	1 PGCA CHICK	P07898 Dermaphag
21	73	9.4	2531	1 NPC1 MOUSE	Q01785 Dermaphag
22	72.5	9.4	309	1 MISA STRPA	P13305 Dermaphag
23	72.5	9.4	423	1 F025 HUMAN	P11753 Dermaphag
24	72	9.3	213	1 H026 YEAST	P15193 Dermaphag
25	72	9.3	381	1 AMPC CITFP	P05193 Dermaphag
26	71	9.2	183	1 S00E HAECO	P05147 Dermaphag
27	71	9.2	469	1 F264 RAT	P05114 Dermaphag
28	70.5	9.1	183	1 PH17 HUMAN	Q08484 Dermaphag
29	70.5	9.1	310	1 MISA STPCP	P13305 Dermaphag
30	70.5	9.1	310	1 MISA STPCP	P13305 Dermaphag
31	70.5	9.1	787	1 ITB6 MOUSE	Q02019 Dermaphag
32	70	9.1	160	1 MD2 CRIGR	P58755 Dermaphag
33	70	9.1	351	1 FTSV MYTIC	Q12851 Dermaphag

RESULT 1

ALL2 DERPPT
ID ALL2 DERPPT STANDARD; PRT; 146 AA.
AC P49278,
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mite Group 2 allergen Der p 2 precursor (Der p II) (DPX).
GN DERP2.
OS Dermatophagoides pteronyssinus (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Analgoidea; Pyroglyphidae;
OC Dermatophagoides.
OX NCBI_TaxID=6956;
RN [1]
PP SEQUENCE FROM N.A.
FX MEDLINE=32255201, PubMed=1141131;
RA Chua K Y, Doyle C.P., Simpson R.J., Turner K.J., Stewart G.A.,
Thomas W.R.;
RT "Isolation of cDNA coding for the major mite allergen Der p II by IgE
plaque immunoassay."
EL Int. Arch. Allergy Appl. Immunol. 91:119-122(1990).
RN [2]
PP SEQUENCE FROM N.A. AND VARIANTS.
FX MEDLINE=1299342, PubMed=1199675;
RA Smith W.A., Hales B.J., Jarnicki A.G., Thomas W.R.;
RT "Allergens of wild house dust mites: environmental Der p 1 and Der p 2
sequence polymorphisms."
EL J. Allergy Clin. Immunol. 107:988-992(2001).
RN [3]
PP PARTIAL SEQUENCE OF 18-57.
FX MEDLINE=89278484, PubMed=733406;
RA Heymann P.W., Chapman M.P., Allford P.C., Fox J.W.,
Platts-Mills T.A.;
RT "Antigenic and structural analysis of group II allergens (Der p II
and Der p II) from house dust mites (Dermatophagoides spp)."
EL J. Allergy Clin. Immunol. 93:1055-1067(1994).
RN [4]
PP STRUCTURE BY NMR.
FX MEDLINE=98409423, PubMed=3737847,
RA Mueller G.A., Benjamin D.C., Rule G.S.;
RT "Tertiary structure of the major house dust mite allergen Der p 2:
sequential and structural homologies."
EL Biochemistry 37:12727-12734(1998).
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- CELLULAR BELONGS TO THE NPC2 FAMILY.
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EMBL: AF176239; AAF64621;

34 70 9.1 593 1 SUMT YEAST
35 69.5 9.0 1245 1 F025 HUMAN
36 69 8.8 469 1 P05147 HAEMONCHUS
37 68 8.8 705 1 DPO2 YEAST
38 67.5 9.7 310 1 MISA STRPN
39 67.5 8.7 631 1 IF2 MICON
40 67 9.7 227 1 IF2 MESAU
41 67 9.7 983 1 CAGE HELPU
42 67 9.7 983 1 CAGE HELPU
43 67 8.7 1460 1 MISA YEAST
44 66.5 8.6 310 1 MISA STRGC
45 66.5 8.6 936 1 EAE CITFR

ALIGNMENTS

P16150 saccharomyc
P07282 silicobac.vit
Q16977 homo sapien
P18121 saccharomyc
P42363 streptococc
Q02815 rickettsia
Q35556 mesocricetu
Q32114 helicobacte
Q18272 helicobacte
P40477 saccharomyc
P42364 streptococc
Q07591 citrobacter

CC Acariformes; Sarcophagidae; Asilidae; Glyptopodidae;
CC Lepidoptera;
CC NCBI TaxID=36936;
CC (1) SEQUENCE FROM N.A.
CC MEDLINE=9377437, PubMed=7649289
CC Schmidt M., van der Ploeg I., Olsson S., van Hage-Hamsten M.,
CC "Amino acid analysis of the mite allergen, Lep 1, identifies two different
CC isoallergens and variants";
CC FEBS Lett. 370:11-14(1995).
CC (2) SEQUENCE OF 141 AA, AMB SEQUENCE OF 141 AA;
CC MEDLINE=95010146, PubMed=7925475;
CC Varela J., Ventas P., Carreira J., Barros J.A., Gimenez Gallego J.,
CC Polo F.;
CC "Primary structure of Lep 1, the main Lepidoglyphus destructor
CC allergen";
CC Eur. J. Biochem. 225:93-98(1994).
CC (3) PARTIAL SEQUENCE OF 17-45;
CC Muthian R., Miller M., Kagen S.;
CC "Barn allergen: Isolation and characterization of the major allergens
CC of storage mites: L. destructor";
CC J. Allergy Clin. Immunol. 97:326-326(1991).
CC (4) SEQUENCE OF 17-34, PubMed=1353122;
CC MEDLINE=9296223, PubMed=1353122;
CC van Hage-Hamsten M., Bergman T., Johansson F., Persson P.,
CC Joernvall H., Haerfast B., Johansson S.G.O.;
CC "N-terminal amino acid sequence of principal allergen of storage mite
CC Lepidoglyphus destructor";
CC Lancet 340:614-614(1992).
CC (5) SUBUNIT: MONOMER.
CC (6) SUBCELLULAR LOCATION: Secreted.
CC (7) SIMILARITY: BELONGS TO THE NPC2 FAMILY.
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CC or send an email to license@sib-sib.ch.
CC (EMBL; X99014; CAA61419.1;)
CC (EMBL; X83875; CAA58755.1;)
CC (EMBL; X83876; CAA58756.1;)
CC (EMBL; X81392; CAA57160.1;)
CC HSP; Q00855; IAHK.
CC InterPro; IPR003172; E1_Dorf2_Dorf2.
CC Pfam; PF02221; E1_Dorf2_Dorf2; 1.
CC Allergen; Polymeric; cm; Repeat; Signal.
CC SIGNAL 1 16 MIE ALLERGEN LEP D 1.
CC CHAIN 17 141 3 X - AA REPEATS OF E V.
CC DOMAIN 24 72 1.
CC REPEAT 64 65 1.
CC REPEAT 68 69 2.
CC REPEAT 72 73 3.
CC BY SIMILARITY.
CC DISULFID 24 133 BY SIMILARITY.
CC DISULFID 37 42 BY SIMILARITY.
CC DISULFID 88 93 BY SIMILARITY.
CC VARIANT 35 35 T > S (IN LEP D 1.02).
CC VARIANT 48 48 E > D (IN LEP D 1.02).
CC VARIANT 53 53 A > D (IN LEP D 1.02).
CC VARIANT 63 63 F I > N (IN LEP D 1.02).
CC VARIANT 75 75 V > I (IN LEP D 1.02).
CC VARIANT 104 104 I > N (IN LEP D 1.02).
CC VARIANT 126 126 S > G (IN LEP D 1.02).
CC VARIANT 126 126 V > I (IN LEP D 1.02).
CC VARIANT 126 126 I > V (IN LEP D 1.02).
CC VARIANT 136 136 V > I (IN LEP D 1.02).
CC VARIANT 136 136 H > E (IN LEP D 1.02).
CC VARIANT 136 136 H > E (IN LEP D 1.02).
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CC (EMBL; X83876; CAA58756.1;)
CC (EMBL; X81392; CAA57160.1;)
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CC VARIANT 75 75 V > I (IN LEP D 1.02).
CC VARIANT 104 104 I > N (IN LEP D 1.02).
CC VARIANT 126 126 S > G (IN LEP D 1.02).
CC VARIANT 126 126 V > I (IN LEP D 1.02).
CC VARIANT 126 126 I > V (IN LEP

[illegible]

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RA Meszaros M.;
RL Thesis (1998), University of Arizona, U.S.A.
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DR EMBL: G31456; M4857/04.1;
DR Accession: G31456; EMBL: G31456;
DR RefSeq: P02221; EMBL: P0221;
KW SIGNAL.
FT CHAIN 1 16 POTENTIAL.
FT STRAND 17 145 ECDYSTEROID REGULATED 16 KDA PROTEIN.
FT DISRUPT 22 137 BY SIMILARITY.
FT DISRUPT 90 97 BY SIMILARITY.
FT CONF_HIT 61 51 N-TERM. (POTENTIAL).
FT LENGTH 141 AA, 1651 No. 1287-1297-1298-1299-1300-1301-1302-1303-1304-1305-1306-1307-1308-1309-1310-1311-1312-1313-1314-1315-1316-1317-1318-1319-1320-1321-1322-1323-1324-1325-1326-1327-1328-1329-1330-1331-1332-1333-1334-1335-1336-1337-1338-1339-1340-1341-1342-1343-1344-1345-1346-1347-1348-1349-1350-1351-1352-1353-1354-1355-1356-1357-1358-1359-1360-1361-1362-1363-1364-1365-1366-1367-1368-1369-1370-1371-1372-1373-1374-1375-1376-1377-1378-1379-1380-1381-1382-1383-1384-1385-1386-1387-1388-1389-1390-1391-1392-1393-1394-1395-1396-1397-1398-1399-1400-1401-1402-1403-1404-1405-1406-1407-1408-1409-1410-1411-1412-1413-1414-1415-1416-1417-1418-1419-1420-1421-1422-1423-1424-1425-1426-1427-1428-1429-1430-1431-1432-1433-1434-1435-1436-1437-1438-1439-1440-1441-1442-1443-1444-1445-1446-1447-1448-1449-1450-1451-1452-1453-1454-1455-1456-1457-1458-1459-1460-1461-1462-1463-1464-1465-1466-1467-1468-1469-1470-1471-1472-1473-1474-1475-1476-1477-1478-1479-1480-1481-1482-1483-1484-1485-1486-1487-1488-1489-1490-1491-1492-1493-1494-1495-1496-1497-1498-1499-1500-1501-1502-1503-1504-1505-1506-1507-1508-1509-1510-1511-1512-1513-1514-1515-1516-1517-1518-1519-1520-1521-1522-1523-1524-1525-1526-1527-1528-1529-1530-1531-1532-1533-1534-1535-1536-1537-1538-1539-1540-1541-1542-1543-1544-1545-1546-1547-1548-1549-1550-1551-1552-1553-1554-1555-1556-1557-1558-1559-1560-1561-1562-1563-1564-1565-1566-1567-1568-1569-1570-1571-1572-1573-1574-1575-1576-1577-1578-1579-1580-1581-1582-1583-1584-1585-1586-1587-1588-1589-1590-1591-1592-1593-1594-1595-1596-1597-1598-1599-1600-1601-1602-1603-1604-1605-1606-1607-1608-1609-1610-1611-1612-1613-1614-1615-1616-1617-1618-1619-1620-1621-1622-1623-1624-1625-1626-1627-1628-1629-1630-1631-1632-1633-1634-1635-1636-1637-1638-1639-1640-1641-1642-1643-1644-1645-1646-1647-1648-1649-1650-1651-1652-1653-1654-1655-1656-1657-1658-1659-1660-1661-1662-1663-1664-1665-1666-1667-1668-1669-1670-1671-1672-1673-1674-1675-1676-1677-1678-1679-1680-1681-1682-1683-1684-1685-1686-1687-1688-1689-1690-1691-1692-1693-1694-1695-1696-1697-1698-1699-1700-1701-1702-1703-1704-1705-1706-1707-1708-1709-1710-1711-1712-1713-1714-1715-1716-1717-1718-1719-1720-1721-1722-1723-1724-1725-1726-1727-1728-1729-1730-1731-1732-1733-1734-1735-1736-1737-1738-1739-1740-1741-1742-1743-1744-1745-1746-1747-1748-1749-1750-1751-1752-1753-1754-1755-1756-1757-1758-1759-1760-1761-1762-1763-1764-1765-1766-1767-1768-1769-1770-1771-1772-1773-1774-1775-1776-1777-1778-1779-1780-1781-1782-1783-1784-1785-1786-1787-1788-1789-1790-1791-1792-1793-1794-1795-1796-1797-1798-1799-1800-1801-1802-1803-1804-1805-1806-1807-1808-1809-1810-1811-1812-1813-1814-1815-1816-1817-1818-1819-1820-1821-1822-1823-1824-1825-1826-1827-1828-1829-1830-1831-1832-1833-1834-1835-1836-1837-1838-1839-1840-1841-1842-1843-1844-1845-1846-1847-1848-1849-1850-1851-1852-1853-1854-1855-1856-1857-1858-1859-1860-1861-1862-1863-1864-1865-1866-1867-1868-1869-1870-1871-1872-1873-1874-1875-1876-1877-1878-1879-1880-1881-1882-1883-1884-1885-1886-1887-1888-1889-1890-1891-1892-1893-1894-1895-1896-1897-1898-1899-1900-1901-1902-1903-1904-1905-1906-1907-1908-1909-1910-1911-1912-1913-1914-1915-1916-1917-1918-1919-1920-1921-1922-1923-1924-1925-1926-1927-1928-1929-1930-1931-1932-1933-1934-1935-1936-1937-1938-1939-1940-1941-1942-1943-1944-1945-1946-1947-1948-1949-1950-1951-1952-1953-1954-1955-1956-1957-1958-1959-1960-1961-1962-1963-1964-1965-1966-1967-1968-1969-1970-1971-1972-1973-1974-1975-1976-1977-1978-1979-1980-1981-1982-1983-1984-1985-1986-1987-1988-1989-1990-1991-1992-1993-1994-1995-1996-1997-1998-1999-2000-2001-2002-2003-2004-2005-2006-2007-2008-2009-2010-2011-2012-2013-2014-2015-2016-2017-2018-2019-2020-2021-2022-2023-2024-2025-2026-2027-2028-2029-2030-2031-2032-2033-2034-2035-2036-2037-2038-2039-2040-2041-2042-2043
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GenCore version 5.1.4 ps 4578
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OM protein: protein search, using sw model

Run on: March 11, 2003, 15:23:43, Search time 40.869 seconds
(without alignments)
326,353 Million cell updates/sec

Title: US-09-877-160-2

Perfect score: 1689

Sequence: 1 MKTIVAIASLLASAVARP.....YFAANIDIMIEEYPYVIL 320

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum pp seq length: 200000000

Post processing: Minimum March 0%

Maximum March 100%

Listing first 45 summaries

Database: SwissProt 40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1689	100.0	320	1	MMAL_DERPT
2	1452.5	86.1	321	1	EJML_EUSMA
3	1425.5	84.4	321	1	MMAL_DERPTA
4	1379.5	22.5	459	1	ORVA_CRYCA
5	1372.5	22.1	322	1	CYSI_HOMAM
6	1368.5	21.8	348	1	PAP3_CARPA
7	1364	21.5	380	1	ACTN_ACTCH
8	1362.5	21.5	343	1	CYSI_DICDI
9	1362	21.4	329	1	CATK_HUMAN
10	1362	21.4	330	1	CATV_PAT
11	1362	21.4	395	1	CATL_BRUPA
12	1360	21.3	323	1	CYCR_HMMAM
13	1359.5	21.3	352	1	PAP2_CARPA
14	1359	21.3	329	1	CATK_MACPA
15	1355.5	21.0	348	1	PAP4_CARPA
16	1353	20.9	279	1	CATV_PABIT
17	1352	20.9	323	1	CATV_MACEE
18	1350	20.7	329	1	CATV_PAT
19	1347.5	20.7	324	1	ACTN_HMMV
20	1344	20.4	324	1	CATV_NPVCF
21	1344	20.4	356	1	CATV_NPVLD
22	1343.5	20.3	345	1	ANAN_ANACO
23	1342	20.2	323	1	CATV_MOCSE
24	1342	20.2	369	1	CYCF_HEMGE
25	1341.5	20.2	450	1	CYCF_TRYBB
26	1339.5	20.1	357	1	CATV_HMMAN
27	1338.5	20.0	343	1	CYSP_PEA
28	1337.5	20.0	324	1	CATV_NPVHC
29	1337	20.0	333	1	CATV_GVCF
30	1336.5	19.9	471	1	CPYR_PYS-A
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32	1335	19.7	323	1	CATV_NPVEM
33	1333.5	19.7	439	1	CYCF_THETA

ALIGNMENTS

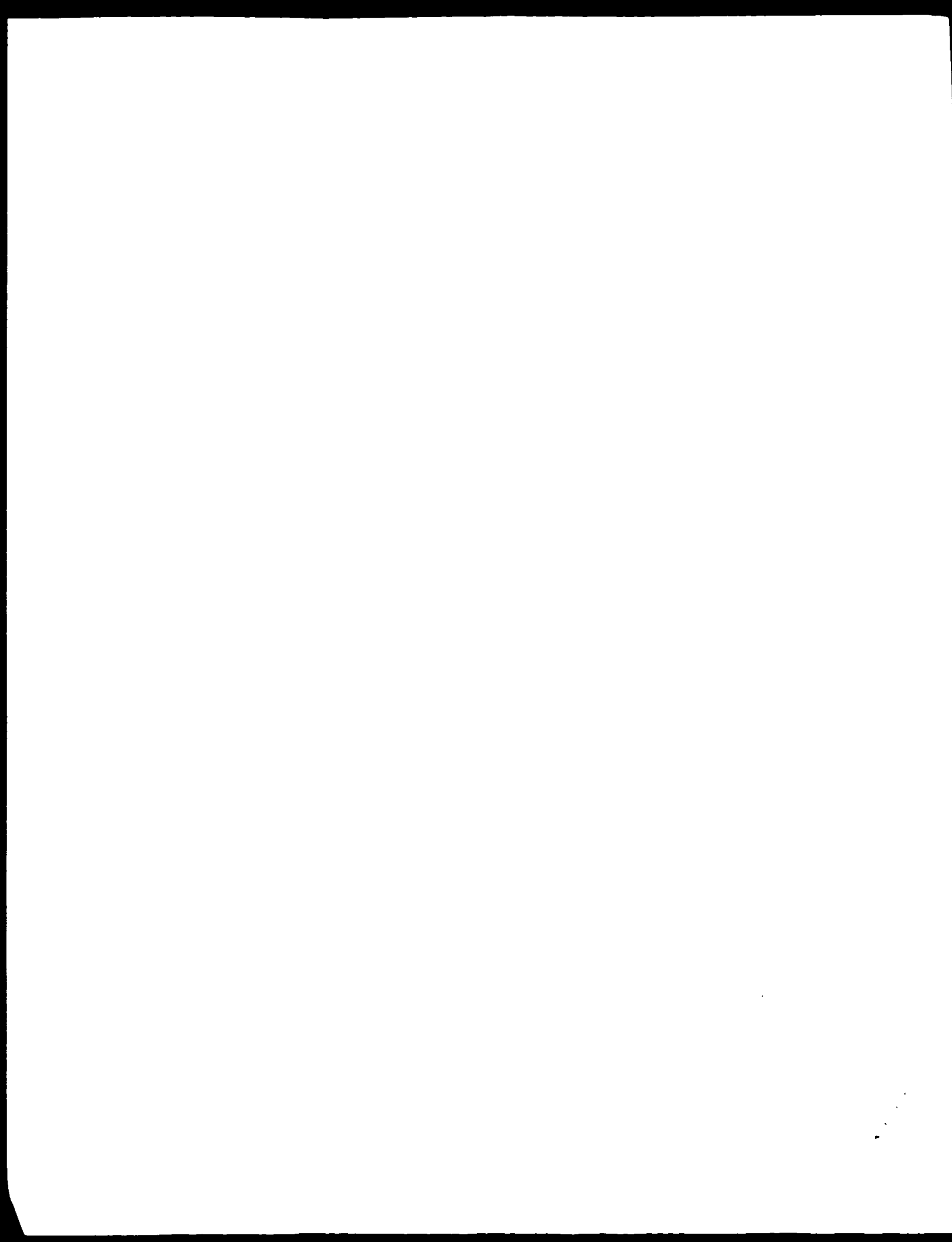
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AC P38176, Q24616;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2003 (Rel. 41, Last annotation update)
DE Major mite fecal allergen Der p 1 precursor (EC 3.4.22.-) (Der p 1).
GN DERP1.
OS Dermatophagoides pteronyssinus (House-dust mite).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
CC Acariformes, Sarcophormes, Astigmata, Analgoidea, Pyroglyphidae;
CC Dermatophagoides.
CX NCPI_TaxID=6656;
RN [1]
PP SEQUENCE FROM N.A., AND POLYMORPHISM.
PV MEDLINE=8157542; PubMed=8154459;
RA Chua K.Y., Kehal P.K., Thomas W.R.;
RT "Sequence polymorphisms of cDNA clones encoding the mite allergen Der p 1.";
RL Int. Arch. Allergy Immunol. 101:364-368(1993).
RN [2]
PP SEQUENCE OF 76-320 FROM N.A.
MEDLINE=88089411; PubMed=3335830;
RA Chua K.Y., Stewart G.A., Thomas W.R., Simpson R.J., Dilworth R.J., Plozza T.M., Turner K.J.;
RT "Sequence analysis of cDNA coding for a major house dust mite allergen, Der p 1. Homology with cysteine proteases.";
PL J. Exp. Med. 167:175-182(1988).
RN [3]
PP SEQUENCE OF 81-176 FROM N.A.
MEDLINE=88114030; PubMed=3276229;
RA Thomas W.R., Stewart G.A., Simpson R.J., Chua K.Y., Plozza T.M., Dilworth R.J., Nisbet A., Turner K.J.;
RT "The binding of mite allergen to the major house dust mite allergen, Der p 1 in Escherichia coli.";
PL Int. Arch. Allergy Appl. Immunol. 85:127-129(1988).
RN [4]
PP SEQUENCE OF 99-127.
MEDLINE=88229138; PubMed=3272999;
RA Lind P., Hansen O.C., Horn N.;
RT "The binding of mite allergen to the major house dust mite allergen, Der p 1.";
PL Int. Arch. Allergy Appl. Immunol. 85:127-129(1988).
RN [5]
PP REVISIONS TO 232 241.
MEDLINE=91216491; PubMed=3031974;
RA Dilworth R.J., Chua K.Y., Thomas W.R.;
RT "Sequence analysis of cDNA coding for a major house dust mite allergen, Der p 1.";
PL Int. Arch. Allergy Appl. Immunol. 85:127-129(1988).
RN [6]
PP SEQUENCE OF 99 308 FROM N.A.
MEDLINE=93103112; PubMed=1483062;

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35 332 19.7 324 1 CATV_PAT
36 332 19.7 344 1 CYSI_DICDI
37 332.5 19.7 443 1 LCPB_LEIME
38 331.5 19.6 324 1 CATV_NPVCF
39 331.5 19.6 346 1 CATV_GVNM
40 330 19.5 462 1 RD21_ARATH
41 329 19.5 273 1 P34_PVEN
42 328 19.4 356 1 CYSI_LVCS
43 328 19.4 444 1 CYSI_LVCS
44 327.5 19.4 328 1 CYS4_BRANA
45 327.5 19.4 335 1 CATV_PIG

G41479 choristoneu
P60782 fatius mrv
P54619 iltyostelli
P36400 leishmania
Q10164 sfgyia pben
Q37172 asstia s-nl
P32297 arabidopsis
P32911 ptylla mrv
Q40143 lycopersico
Q26834 leishmania
P25251 brassica na
Q46427 sus scrofa


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FT DISULPID 270 319 BY SIMILARITY.
CATHESPIN L14 114 B-LIKE (SCN) (SPININ)
SEQUENCE 28 AA, 3768 MW, AASPPRESENTATION TEMPO,
Quer, Natch 1141, Score 100, 10. Length 300,
Best local similarity 1141, Field Name CATHESPIN
Matches 9, Conservative 40, Mismatches 130, Indels 24, Gaps 11
QV 1 MPVLAACCAACATCAFISSTIETEEAFAPWATELLAEAFEPKPVV
| | | | | | | | | | | | | | | | | | | | | |
Db 4 DNVLDLP VNGCALVEELIETWLVAVTFFVYVNSPTETSEFVWFPHRIG
| | | | | | | | | | | | | | | | | | | | | |
QV 15 QVLSL ALNELLELEENRNENALAHILLAEFEFNEEACAGHENE 119
| | | | | | | | | | | | | | | | | | | | | |
Db 60 NEELGTHTEELAEAGCGTGEVTWGLSFLVSHLS HELLINGWEEST 119
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QV 110 AVDTETETETNTMGGCTGWAFQWATERVAIAVENLDEAFRLM APRU 119
| | | | | | | | | | | | | | | | | | | | | |
Db 118 EITTFVETVTPPELQQWAWLGVVALSLFYVDFVNLNQVMTVADGS 119
| | | | | | | | | | | | | | | | | | | | | |
QV 174 THTTETETETTN TNNERTTETVWATEREF SPANDETETNTTYNDPFR 226
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Db 179 CLLETNTAFATVDEMESELAVTVELERWTHTVPAAFTLSPEETEDFAIF 179
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QV 200 ELAACHALLAVLIMILLAFNRNSETTEREVIENTV HASTIVINDAGATVI 295
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Db 209 EGAAET EPVVAE ALLDLEL SHOTTER INDELAVAVSYGTPTFWI 334
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QV 228 TENDKTETNENGNVFAM 305
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Db 295 KNSAGENVGNKGVMARN 314
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RESULT 11
CATL BRUGA
ID CATL BRUGA STANARD, EST, 300 AA.
OC 0:V473;
DI 15 JUL 1999 (Sep. 98, Created).
DT 15-JUL-1999 (Sep. 98, Last sequence update)
DE CATHESPIN L14 114, last updated 15 Jul 1999.
DE CATHESPIN L-like precursor (EC 3.4.22.15).
CC Bugia phangi.
CC P. Arizata, Madrid, Spain.
CC Cheliceridae, Elaejia.
CX NCBI TaxID=6280;
RN [1] -
RP SEQUENCE FROM N.A.
RA Kaiser F.M., Huang X., Britton C., Wernert J.H.
RT "Cathespin L-like cysteine protease from Bugia phangi third stage larvae."
RL C.M. Wang (last name), The PowerPackProtein database
RN [2]
RP 3D-STRUCTURE MODELING OF 194-295.
RP Seiler P.M., Chen Y., Cohen R.E., McMillan J.H.
RP "Structural studies of Proteasins phangi third stage larvae cytosolic proteases".
RL Submitted (JUL-1998) to the PDB data bank.
CC 1 - CATHESPIN ACTIVITY Specificity, also that of papain. As compared to Cathespin B, cathespin L exhibits higher activity towards protein substrates, but has little affinity to 2 Arg Arg
CC toward and no fused-indicetase activity.
CC 1 - SIMILARITY RESULTS TO RELEVANT FAMILY 11
CC This SwissProt entry is "phagi". It is produced through a collaboration between the Swiss Institute of Bioinformatics and the pest operation at the European Bioinformatics Institute. There are no restrictions on its use by any other institutions as long as its current is in the way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/seqdb/doc/copy_email_to_licenseist.html).
CC or send an email to licenseist@ebi.ac.uk.
CC EMBL, AF021913, AAP09071,
DR ECB, IBBN, 23 JUL 98.
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US 08 461-809-10

Query Match: 99.23; Score 1676; EE 1; Length 320;
 Best Local Similarity 99.18; Pct 5.5e-169;
 Matches 317; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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 Db 1 MKVLAAGLALSAVYARPPSSINTEEFYFAFNKSVATFEFFFAAPPPFESVYVQCN 60

Q: 61 GGAINHLSLSLDEPKPFMSAEAFELHKTQFDLNATNCSINONAFIDLPOMTV 120
 Db 61 GGAINHLSLSLDEPKPFMSAEAFELHKTQFDLNATNCSINONAFIDLPOMTV 120

Q: 121 TPIRMQGGGSCWAFSGVAATESAYLAVNQSLLAEELACASQHSCHGDIIPGGLEY 180
 Db 121 TPIRMQGGGSCWAFSGVAATESAYLAVNQSLLAEELACASQHSCHGDIIPGGLEY 180

Q: 181 IQHNGVVQESYRYVAPEQSCPPNAQPPSISNYQIYPPNNVNEIKALAQTHSAIAVII 240
 Db 181 IQHNGVVQESYRYVAPEQSCPPNAQPPSISNYQIYPPNNVNEIKALAQTHSAIAVII 240

Q: 241 GIKELDAFRHYDGETTIQRENGYQENYHVNIVGYNAGGVYVWIVRNSWUTNMGDNGYG 300
 Db 241 GIKELDAFRHYDGETTIQRENGYQENYHVNIVGYNAGGVYVWIVRNSWUTNMGDNGYG 300

Q: 301 YFAANIDLMIMIEEYPYVWIL 320
 Db 301 YFAANIDLMIMIEEYPYVWIL 320

RESULT 4

US 08-461 441-10
 : Sequence 10, Application US/08461441
 : Patent No. 5773062
 : GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM

DERMATOPHAGOIDES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COMPANY

STREET: 60 STATE STREET, SUITE 510

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,441

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/945,288

FILING DATE: 10 SEPTEMBER 1992

APPLICATION NUMBER: US 580,655

FILING DATE: 11 SEPTEMBER 1990

APPLICATION NUMBER: US 458,642

FILING DATE: 13 FEBRUARY 1990

ATTORNEY/AGENT INFORMATION:

NAME: MANDRAGOURAS, AMY E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO. 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 320 amino acids

TYPE: amino acid

TOPOLOGY: linear

TYPE: amino acid
 TOPOLOGY: linear
 MEDIUM TYPE: floppy disk
 US 08-461-441-10

Query Match: 99.23; Score 1676; EE 1; Length 320;

Best Local Similarity 99.18; Pct 5.5e-169;

Matches 317; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Q: 1 MKVLAAGLALSAVYARPPSSINTEEFYFAFNKSVATFEFFFAAPPPFESVYVQCN 60
 Db 1 MKVLAAGLALSAVYARPPSSINTEEFYFAFNKSVATFEFFFAAPPPFESVYVQCN 60

Q: 61 GGAINHLSLSLDEPKPFMSAEAFELHKTQFDLNATNCSINONAFIDLPOMTV 120
 Db 61 GGAINHLSLSLDEPKPFMSAEAFELHKTQFDLNATNCSINONAFIDLPOMTV 120

Q: 121 TPIRMQGGGSCWAFSGVAATESAYLAVNQSLLAEELACASQHSCHGDIIPGGLEY 180
 Db 121 TPIRMQGGGSCWAFSGVAATESAYLAVNQSLLAEELACASQHSCHGDIIPGGLEY 180

Q: 181 IQHNGVVQESYRYVAPEQSCPPNAQPPSISNYQIYPPNNVNEIKALAQTHSAIAVII 240
 Db 181 IQHNGVVQESYRYVAPEQSCPPNAQPPSISNYQIYPPNNVNEIKALAQTHSAIAVII 240

Q: 241 GIKELDAFRHYDGETTIQRENGYQENYHVNIVGYNAGGVYVWIVRNSWUTNMGDNGYG 300
 Db 241 GIKELDAFRHYDGETTIQRENGYQENYHVNIVGYNAGGVYVWIVRNSWUTNMGDNGYG 300

Q: 301 YFAANIDLMIMIEEYPYVWIL 320
 Db 301 YFAANIDLMIMIEEYPYVWIL 320

RESULT 5

US 93-08518-10
 : Sequence 10, Application PC/TUS9308518
 : GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM

DERMATOPHAGOIDES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COMPANY

STREET: 60 STATE STREET, SUITE 510

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PC/TUS93/08518

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/945,288

FILING DATE: 10 SEPTEMBER 1992

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: MANDRAGOURAS, AMY E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IPC-010CC (IMI-024)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO. 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 320 amino acids

TYPE: amino acid

TOPOLOGY: linear


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; INFORMATION FOR SEQ ID NO: 6:
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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 321 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE LIFE: protein
US 08 462-831-6

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Query Match 84.4%; Score 1425.5; DB 1; Length 321;
Best Local Similarity 92.9%; Pred. NC. 26.142;
Matches 266; Conservative 25; Mismatches 29; Indels 1;

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RESULT 8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,831
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,288
FILING DATE: 18 SEPTEMBER 1992
APPLICATION NUMBER: US 580,655
FILING DATE: 11 SEPTEMBER 1990
APPLICATION NUMBER: US 458,642
FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGORAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOC#ET NUMBER: IPC-01000 (IMI-024)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US 08-462-831-2

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Query Match: 77.78; Score 1313; DB 1; Length 245;
Res: Local Similarity 29.24; Pred. No. 1,le-130;
Matches 243; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 76 KNRLMSAEFEHKTQEDNARINATSNINAPAEIQRQMTVTPIPW-220SCWAF 135
Db 1 KNRLMSAEFEHKTQEDNARINATSNINAPAEIQRQMTVTPIPW-220SCWAF 135

Qy 136 SGVAATESAVLAVPNQSELEAEELVCAQCHQCHJITIPGIEYIGHNGVWQESYRYV 195
Db 61 SGVAATESAVLAVPNQSELEAEELVCAQCHQCHJITIPGIEYIGHNGVWQESYRYV 120

Qy 176 AREQCTSPNHPREPIENYCIITPPWVNIPEALQTHSAIAVIGIKLLAFHNYDGT 255
Db 121 AREQCTSPNHPREPIENYCIITPPWVNIPEALQTHSAIAVIGIKLLAFHNYDGT 180

Qy 206 IIGKNGTQPHAVNIVGKSNAGVGVWIVPNSWPNWLNWNGVYGFANILMMIEEYP 315
Db 191 IIGKNGTQPHAVNIVGKSNAGVGVWIVPNSWPNWLNWNGVYGFANILMMIEEYP 240

Qy 316 YWVIL 320
Db 241 YWVIL 245

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Search completed: March 12, 2003, 13:27:24
Job time : 46.4147 secs

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      : LQVWPTGCAHCEFFPPFVPELVNCHSEEDLHNSVFTFLPALEAFATHTTAPTEHPASLSG 60
    Cy 78 LEVAVPSTPLDIAQHWPYLYNFYKLTNTITFTWTHPTFAFSSEHWVATVTCTTTWACA 129
    De 81 LEIDVPDITNAHQEWKDTVFQQQADIVFWWRNPKTAPSSSHVVTVPLIQNVYLACA 120
    Cy 138 IATHAKTPD 145
    |||||
    Ft 171 IATHSTFP 129
    |||||

RESULT 5
A61501
allergen Der f II - house-dust mite (Dermatophagoides farinae) (fragment)
C:Species: Dermatophagoides farinae
C:Date: 07-Oct-1994 #sequence revision 07-Oct-1994 #text_change 13-Sep-1999
C:Accession: A61501
R:Trudinger, M.; Chua, K.Y.; Thomas, W.R.
J Clin. Exp. Allergy 21, 33-37, 1991
A:Title: cDNA encoding the major mite allergen Der f II.
A:Reference number: A61501; MIDB:01215495; PMID:2021476
A:Accession: A61501
A:Status: preliminary, not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-129 <TP>S
C:Superfamily: allergen Der p II

Query Match          80.7% Score 624   DB 2: Length 129;
Best Local Similarity 87.6%; Prod.No:6.2e-55; Indels 0; Gaps
Matches 113, Conservative 113, Miscellaneous 5; Indels 0; Gaps

Cy 14 DEAVVTCATSEIFFPVVEVDECHTEETFTTFSPPTFAVTAHQCTTAPTEHPASLSG 77
|||
Ft 17 VAVELANNEIFKAWVDEHSDFEHLHVSGLAAHAEATATTEHPASLSG 63
|||

Cy 79 LEVVVGPDINACHVWVCVLVQLVQLVGVYKVIYNVSLINPSSENVTUTVKWMTSGWLACA 137
|||
Ft 11 LEVIEVPTTARHPVPTFLVVAETLCATATWMTTAPTEHPASLSG 63
|||

Cy 138 IATHAKTPD 145
    |||||
    Ft 121 IATHAKTPD 129
    |||||

RESULT 6
S66400
allergen Lep d 101 precursor (lepidoglyphus destructor
C:Species: Lepidoglyphus destructor
C:Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 23-Feb-1999
C:Accession: S66500; S49727; S66014
R:Schmidt, M.; Olsson, S.J; van der Ploeg, J.; van Hage-Hamsten, M.
FEBS Lett. 370, 11-14, 1995
A:Title: cDNA analysis of the mite allergen Lep d 1 identifies two different
A:Reference number: S66400; MIDB:06377437; PMID:7649268
A:Accession: S66500
A:Molecule type: mRNA
A:Residues: 1-141 <SCH>
A:Cross-references: EMP1:060014; MIDB:060014; PIN:06A6149 1; PID:0604422
F:E-Varela, C.; Ventas, F.; Carricra, J.; Barba, T.A.; Gilmer-Gallego, C.
Eur J Biochem 225, 93-98, 1994
A:Title Primary structure of Lep d 1, the main lepidoglyphus destructor a
A:Reference number: S49727, MIDB:05010146, PMID:7056475
A:Accession: S49727
A:Molecule type: mRNA
A:Residues: 44-141 <VAM>
A:Cross references: EMBL:X91203, MIDB:35EM142, PIN:06A6149 1; PID:0604450
A:Accession: S56034
A:Molecule type: protein
A:Residues: 17-140 <VAR>
A:Superfamily: Asp. 43 Arg., 45-Ile, 104-Asn, 106-Gly and 126-Val were also fou
C:Superfamily: allergen Der p II
F:Lic/Domin: signal sequence status Predicted <SIG>
MIDB:17140/Predict: allergen lep d 1 01 #status experimental <VAR>
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Query Match 36.0%; Score 278.5; DB 2; Length 141;
 Best Local Similarity 37.1%; Pred No. 1.8e-26;
 Matches 53; Conservative 33; Mismatches 54; Indels 3; Gaps 3;

QY 2 MYH10LGLLVAAVASEGVVPTTANRFFPPVLPVCHCEFCIFHPSKPCLEAVPEAN 61
 DB 1 MMFEIALPALVAVASAGKMTFFKGGVPTREINITSQSG-DTCVHPGQVMTLEAVPEAN 59
 QY 62 CRTPTAFIEFPAICTELEVEVETIFRNACVWVGLFVAVLENDIDYTNWVNIHPECEV 121
 DB 60 GDAARVIFVLA-AVAHILVDSLEFTEGGLYFIPVFFPAALHIFSTITFAITFAVE A 118
 QY 122 VVTVWVSGDGVLAATIAHAKI 144
 DB 119 DVTAEIIGVSHVWACG-THGQV 140

RESULT 7
 S66499
 allergen Lep d 1.02 protein, Lepidodermis leprosa
 C:Species: Lepidodermis destructor
 C:Date: 12 Mar 1997 #sequence_revision 10 Mar 1997 #text_change 10 Sep 1998
 C:Accession: S66499
 R:Schmidt, M., Stöckli, C., van der Flier, J., van Hage-Hamsten, M.
 FEBS Lett. 376, 11-14, 1995
 A:Title: cDNA analysis of the mite allergen Lep d 1 identifies two different isoallergens
 A:Reference number: S66499; MUID:95377437; PMID:7649288
 A:Accession: S66499
 A:Molecule type: mRNA
 A:Residues: 141<824>
 A:Cross-references: EMBL:X83875; NID:9999457; PIDN:CAAS4875.1; PID:9999458
 C:Superfamily: allergen Der p II
 F11 16/06/01 signal sequence #status predicted #SIGP
 F17 141/51 1.02 allergen Lep d 1.02 beta is predicted #WAT

Query Match 35.1%; Score 274.5; DB 2; Length 141;
 Best Local Similarity 36.4%; Pred No. 4.5e-20;
 Matches 52; Conservative 32; Mismatches 55; Indels 3; Gaps 3;

QY 2 MYH10LGLLVAAVASEGVVPTTANRFFPPVLPVCHCEFCIFHPSKPCLEAVPEAN 61
 DB 1 MMFEIALPALVAVASAGKMTFFKGGVPTREINITSQSG-DTCVHPGQVMTLEAVPEAN 59
 QY 62 CRTPTAFIEFPAICTELEVEVETIFRNACVWVGLFVAVLENDIDYTNWVNIHPECEV 121
 DB 60 GDAARVIFVLA-AVAHILVDSLEFTEGGLYFIPVFFPAALHIFSTITFAITFAVE A 118
 QY 122 VVTVWVSGDGVLAATIAHAKI 144
 DB 119 DVTAEIIGVSHVWACG-THGQV 140

RESULT 8
 I38365
 epididymal secretory protein, human
 C:Species: Homo sapiens (man)
 C:Date: 01-Nov-1976 #sequence_revision 31 Nov 1997 #text_change 1 Oct 2000
 C:Accession: I38365; S25641
 P:Kruhl, N., Ivell, P., Osterhoff, C., Kirchhoff, C.
 Mol. Reprod. Dev. 34, 16-24, 1993
 A:Title: Region specific variation of gene expression in the human epididymis as revealed
 A:Reference number: I38365; MUID:93119459; PMID:8418812
 A:Accession: I38365
 A:Molecule type: mRNA
 A:Residues: 145<824>
 A:Cross-references: EMBL:X67698; NID:937476; PIDN:CAAM7928.1; PID:937477
 A:Note: submitted to the EMBL Data Library, August 1992
 C:Superfamily: allergen Der p II

Matches 35; Conservative 26; Mismatches 46; Indels 10; Gaps 5;

QY 6 LLSLLVAAVAPQGVVVFETARHE IFFVLAIFRHEFFIHRFFIFPALEMANON 63
 DB 9 LLSLLVAAVAPQGVVVFETARHE IFFVLAIFRHEFFIHRFFIFPALEMANON 66
 QY 64 TTAKEIFKASIGLEVEVEVETIFRNACVWVGLFVAVLENDIDYTNWVNIHPECEV 119
 DB 67 LLSLLVAAVAPQGVVVFETARHE IFFVLAIFRHEFFIHRFFIFPALEMANON 118

RESULT 9
 I53929
 epididymal secretory protein 14, Crabs eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 01 Jul 1997 #sequence_revision 01 Jul 1997 #text_change 01 Jul 1997
 C:Accession: I53929
 R:Perry, A.C., Jones, R., Hall, L.
 Gene 153, 291-292, 1995
 A:Title: The monkey ESF14.6 mRNA, a novel transcript expressed at high levels in the ep
 A:Reference number: I53929; MUID:916747; PMID:7575608
 A:Accession: I53929
 A:Status: preliminary; translated from GB/EMBL/DBRJ
 A:Molecule type: mRNA
 A:Residues: 141<824>
 A:Cross-references: EMBL:X76134; NID:9794070; PIDN:CAAS5013.1; PID:9794071
 C:Superfamily: allergen Der p II

Query Match 15.9%; Score 123; DB 2; Length 151;
 Best Local Similarity 29.9%; Pred No. 6e-05;
 Matches 35; Conservative 26; Mismatches 46; Indels 10; Gaps 5;

QY 6 LLSLLVAAVAPQGVVVFETARHE IFFVLAIFRHEFFIHRFFIFPALEMANON 63
 DB 9 LLSLLVAAVAPQGVVVFETARHE IFFVLAIFRHEFFIHRFFIFPALEMANON 66
 QY 64 TTAKEIFKASIGLEVEVEVETIFRNACVWVGLFVAVLENDIDYTNWVNIHPECEV 119
 DB 67 LLSLLVAAVAPQGVVVFETARHE IFFVLAIFRHEFFIHRFFIFPALEMANON 118

RESULT 10
 T32408
 hypothetical protein R148.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 25-Oct-1999 #sequence_revision 25 Oct 1999 #text_change 29 Oct 1999
 C:Accession: T32408
 R:Lee, T.T., Kemp, K., Scheet, P.
 submitted to the EMBL Data Library, September 1997
 A:Description: The sequence of C. elegans cosmid R149.
 A:Reference number: T32408
 A:Accession: T32408
 A:Status: preliminary; translated from GB/EMBL/DBRJ
 A:Molecule type: DNA
 A:Residues: 1-186<187>
 A:Cross-references: EMBL:AF025467; FLM:AA51144.1; GDB:R38442; JEMR:R148.6
 A:Experimental source: strain Bristol N2; clone R148
 C:Genetics:
 A:Gene: CESP:R148.6
 A:Map position: 3
 A:Annotations: 32/2; 122/1

Query Match 14.9%; Score 115.5; DB 2; Length 186;
 Best Local Similarity 23.4%; Pred No. 0.0043;
 Matches 36; Conservative 38; Mismatches 71; Indels 9; Gaps 5;

QY 2 MYH10LGLLVAAVASEGVVPTTANRFFPPVLPVCHCEFCIFHPSKPCLEAVPEAN 61
 DB 1 MMFEIALPALVAVASAGKMTFFKGGVPTREINITSQSG-DTCVHPGQVMTLEAVPEAN 59
 QY 62 CRTPTAFIEFPAICTELEVEVETIFRNACVWVGLFVAVLENDIDYTNWVNIHPECEV 121
 DB 60 GDAARVIFVLA-AVAHILVDSLEFTEGGLYFIPVFFPAALHIFSTITFAITFAVE A 118

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The first part of the paper discusses the importance of the study and the objectives of the research. It highlights the need for a comprehensive understanding of the subject matter and the role of the researcher in this process. The second part of the paper presents the methodology used in the study, including the data collection methods and the analysis techniques. The third part of the paper discusses the results of the study and the conclusions drawn from the findings. The final part of the paper provides a summary of the key points and offers suggestions for future research.

The study was conducted in a systematic and rigorous manner, following the principles of scientific research. The data was collected from a large sample of participants, and the results were analyzed using advanced statistical techniques. The findings of the study are presented in a clear and concise manner, allowing for a thorough understanding of the subject matter. The conclusions drawn from the findings are based on a careful analysis of the data and are supported by the results of the study.

The study has several limitations, which are discussed in the paper. These limitations include the sample size, the duration of the study, and the potential for bias. Despite these limitations, the study provides valuable insights into the subject matter and contributes to the existing body of knowledge. The findings of the study are discussed in the context of the current research and are compared with the results of other studies.

The study has several implications for practice and policy. The findings of the study suggest that there is a need for further research in this area, and that the results of the study can be used to inform decision-making. The study also highlights the importance of the role of the researcher in this process and the need for a comprehensive understanding of the subject matter.

In conclusion, the study provides a comprehensive understanding of the subject matter and contributes to the existing body of knowledge. The findings of the study are presented in a clear and concise manner, allowing for a thorough understanding of the subject matter. The conclusions drawn from the findings are based on a careful analysis of the data and are supported by the results of the study.

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☐ Helped examiner better understand the invention.

☐ Helped examiner better understand the state of the art in their technology.

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(journal articles, conference proceedings, new product announcements etc.)

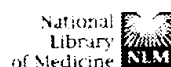
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1: J Interferon Cytokine Res 2000 Dec;20(12):1057-63

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Modulation of IgE response and cytokine production in Peyer's patches and draining lymph nodes in sensitized mice made tolerant by oral dust mite administration.

Maciel M, Fusaro AE, Duarte AJ, Sato MN.

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Laboratorio de Alergia e Imunologia Clínica e Experimental/LIM-56, Faculdade de Medicina da Universidade de São Paulo-Brasil.

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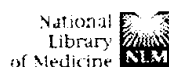
Such allergic diseases as rhinitis and asthma are IgE-mediated type I reactions and are controlled primarily by Th2 cells. One of the major dust mites, *Dermatophagoides pteronyssinus* (Dp), is considered to cause allergic reactions. Oral tolerance, largely used to modulate immune response, opens the possibility of modulating Th2 allergic responses. We observed downmodulation of total and specific IgE antibody levels as well as the number of specific IgE-secreting cells with Dp feeding in previously sensitized mice. Analysis of the cytokine profile in mucosal lymphoid tissues in the protocol revealed altered patterns of interferon-gamma (IFN-gamma), interleukin-5 (IL-5), and transforming growth factor-beta (TGF-beta) secretion in Dp-fed animals. The results suggest that both the Th and B cell populations are modulated in mice made tolerant by oral Dp feeding. Understanding the mechanisms at the mucosal level that underlie oral tolerance can improve its use in allergy immunotherapy.

PMID: 11152571 [PubMed - indexed for MEDLINE]

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1: Experientia 1991 Sep 15;47(9):905-12

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Production of pharmaceutical proteins in milk.

Wilmut I, Archibald AL, McClenaghan M, Simons JP, Whitelaw CB, Clark AJ.

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AFRC Institute of Animal Physiology and Genetics Research, Roslin, Midlothian, Scotland.

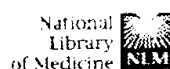
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There is every reason to expect that it will be possible within the next few years to begin to use farm animals to produce large quantities of some of the human proteins that are needed for the treatment of disease. Revolutionary new opportunities for the production of novel proteins in milk have been created by the development of methods for gene transfer. Exploitation of these opportunities depends upon selection and cloning of milk protein genes and identification of the sequences that govern tissue specific hormonally induced expression in the mammary gland. Studies with three genes, ovine beta-lactoglobulin, rat beta-casein and whey acidic protein of rat and mouse, suggest that they may all meet this requirement. Fragments of the ovine beta-lactoglobulin, murine whey acidic protein and rabbit beta-casein genes have directed production of novel proteins in the milk of transgenic mice, sheep, rabbits and pigs. The proteins were biologically active and usually co-migrated with authentic proteins. In early experiments, protein concentration was low, but our recent observations suggest that fusion genes containing genomic clones direct production of concentrations of protein that are suitable for commercial exploitation. In the longer term, two approaches may offer the potential of more reliable expression. Control elements capable of directing expression that is independent of site of insertion of the gene, but dependent on the number of copies of the gene, have been identified for a small number of genes. The availability of such elements for the milk protein genes would increase the reliability of gene expression considerably. Alternatively, targeted mutation of genes may allow the insertion of coding sequences within an existing gene so avoiding position effects.

Publication Types:

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- Review, Tutorial

PMID: 1915774 [PubMed - indexed for MEDLINE]



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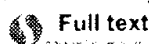
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☐ 1: Immunology 1998 Oct;95(2):193-9

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Oral tolerance induced to house dust mite extract in naive and sensitized mice: evaluation of immunoglobulin G anti-immunoglobulin E autoantibodies and IgG-IgE complexes.

Sato MN, Carvalho AF, Silva AO, Maciel M Jr, Fusaro AE, Duarte AJ.

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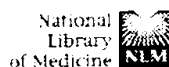
Laboratorio de Imunogenetica e Transplante Experimental LIM-56, Faculdade de Medicina da USP (FMUSP), Sao Paulo, Brasil.

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We investigated the effect on specific antibody response of naive and sensitized mice orally administrated with low (0.25 mg) or high (10.0 mg) doses of *Dermatophagoides pteronyssinus* (Dp) extract. We also examined the effect of oral administration of Dp on the production of autoantibodies to immunoglobulin G (IgG) and immunoglobulin E (IgE). Naive and sensitized mice both showed a marked down-regulation of IgE antibody production, regardless of the dose of Dp. We also detected an inhibitory effect of the total IgE levels and the allergen-specific IgG1, IgG2a and IgG2b antibody response in sensitized mice given the low dose of Dp. In contrast, high doses of Dp stimulated IgG1 antibody production in both naive and sensitized animals. In addition, the oral tolerance induction protocol stimulated anti-F(ab')₂gamma and anti-Fcgamma autoantibody production. Evaluation of IgG anti-IgE autoantibodies by a direct enzyme immunoassay (EIA) revealed the presence of these autoantibodies, predominantly of the IgG1 isotype, specifically in those animals fed with the high dose. In contrast, IgG-IgE complexes, determined by EIA using immobilized anti-IgE antibodies, were detected mainly in sera of control animals. The autoantibody anti-IgE specificity was tested against IgE-TNP and IgE-DANSYL murine proteins and revealed different inhibition profiles, suggesting the action of heterogeneous subpopulations of autoantibodies. Taken together, our results show that the oral tolerance protocol with Dp was able to modulate the production of allergen-specific IgE antibodies in both naive and sensitized animals. In addition, we suggest that anti-IgE autoantibodies participate in the modulation of allergic response triggered by oral tolerance protocols.

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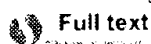
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1: Immunology 1999 Nov;98(3):338-44

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Low dose of orally administered antigen down-regulates the T helper type 2-response in a murine model of dust mite hypersensitivity.

Sato MN, Carvalho AF, Silva AO, Maciel M Jr, Fusaro AE, Duarte AJ.

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Laboratorio de Alergia e Imunologia Clinica e Experimental-LIM 56, Faculdade de Medicina da Universidade de Sao Paulo, Sao Paulo, Brazil.

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One of the main goals of immunotherapy of allergic diseases is the down-regulation of the type I hypersensitivity reaction. We investigated in this study the effect of oral administration of varying doses (0.25, 1.0, 4.0 and 10 mg) of dust mite extract (*Dermatophagoides pteronyssinus*, Dp) in sensitized A/Sn mice. A marked decrease of the allergen-specific immunoglobulin E (IgE) response was observed with all antigen doses. The mice orally tolerized with low Dp dose (0.25 mg) had a significant decrease in the total serum IgE and in the immunoglobulin G1 (IgG1), IgG2a and IgG2b antibody levels. The higher Dp dose (10.0 mg), however, enhanced the IgG1 antibody response, suggesting the stimulation of a pre-existing immune response of the sensitized animals. Animals fed with the low Dp dose had a significant decrease in the frequency of interleukin-4 (IL-4) secreting cells. These animals also showed a significant decrease in the frequency of Dp-specific IgE- and IgG1-positive plasma cells. Our data suggest that feeding dust mite extract to Dp-sensitized mice down-regulates the development of type I hypersensitivity, by inhibition of the T helper 2 response.

PMID: 10583591 [PubMed - indexed for MEDLINE]

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the 1990s, the number of people in the UK who are aged 65 and over has increased from 10.5 million to 12.5 million, and the number of people aged 75 and over has increased from 4.5 million to 6.5 million (Office of National Statistics 2000). The number of people aged 65 and over is projected to increase to 15.5 million by 2020, and the number of people aged 75 and over to 8.5 million (Office of National Statistics 2000). The increase in the number of people aged 65 and over is expected to be due to a combination of factors, including a decline in the birth rate, a decline in the death rate, and a decline in the rate of emigration.

The increase in the number of people aged 65 and over is expected to have a significant impact on the UK's health and social care system. The number of people aged 65 and over who are in need of health and social care services is expected to increase significantly in the coming years. This is due to a number of factors, including the fact that older people are more likely to have chronic health conditions, and the fact that older people are more likely to need help with everyday activities. The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's economy. The number of people aged 65 and over who are in the workforce is expected to decline significantly in the coming years, which will lead to a shortage of workers in many sectors of the economy.

The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's housing market. The number of people aged 65 and over who own their own home is expected to decline significantly in the coming years, which will lead to a shortage of homes for older people. This is due to a number of factors, including the fact that older people are more likely to have a lower income, and the fact that older people are more likely to need help with everyday activities. The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's transport system. The number of people aged 65 and over who are in the workforce is expected to decline significantly in the coming years, which will lead to a shortage of workers in many sectors of the transport system.

The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's education system. The number of people aged 65 and over who are in the workforce is expected to decline significantly in the coming years, which will lead to a shortage of workers in many sectors of the education system. This is due to a number of factors, including the fact that older people are more likely to have a lower income, and the fact that older people are more likely to need help with everyday activities. The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's health and social care system. The number of people aged 65 and over who are in need of health and social care services is expected to increase significantly in the coming years.

The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's economy. The number of people aged 65 and over who are in the workforce is expected to decline significantly in the coming years, which will lead to a shortage of workers in many sectors of the economy. This is due to a number of factors, including the fact that older people are more likely to have a lower income, and the fact that older people are more likely to need help with everyday activities. The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's housing market. The number of people aged 65 and over who own their own home is expected to decline significantly in the coming years, which will lead to a shortage of homes for older people.

The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's transport system. The number of people aged 65 and over who are in the workforce is expected to decline significantly in the coming years, which will lead to a shortage of workers in many sectors of the transport system. This is due to a number of factors, including the fact that older people are more likely to have a lower income, and the fact that older people are more likely to need help with everyday activities. The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's education system. The number of people aged 65 and over who are in the workforce is expected to decline significantly in the coming years, which will lead to a shortage of workers in many sectors of the education system.

The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's health and social care system. The number of people aged 65 and over who are in need of health and social care services is expected to increase significantly in the coming years. This is due to a number of factors, including the fact that older people are more likely to have chronic health conditions, and the fact that older people are more likely to need help with everyday activities. The increase in the number of people aged 65 and over is also expected to have a significant impact on the UK's economy. The number of people aged 65 and over who are in the workforce is expected to decline significantly in the coming years, which will lead to a shortage of workers in many sectors of the economy.